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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 12, 2004, 06:12:47; Search time 0.461066 Seconds (without alignments) 1043.144 Million cell updates/sec Run on: Title:

US-09-890-463-1 21 1 SVIAK 5 Perfect score: Scoring table: Sednence:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	division	-			hypothetical prote	Ġ.	hypothetical prote	hypothetical prote	probable sugar-pho	hypothetical prote	hypothetical prote	tetR family bacter	transcription regu	UL1 protein - huma	basal-body rod mod	probable membrane-	nonstructural prot	probable S-adenosy		ribosomal protein	pancreatic elastas	-acylg		mating type protei	probable glycosylt	O)	prot		DNA-directed DNA p
ΩI	AI29				AF1931							A97665		WMBEHG			MINVUPT		G81674	D64217	ELRT2	T5012			A95910		F9776	S480	A2711
DB	1																	-1											
Length	86	86	132	171	181	188	194	197	200	203	203	219	219	224	236	243	250	263	266	268	271	279	282	293	301	305	331	335	335
장성	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	00	00	00	00	00	100.0	100.0	100.0		100.0	0	00	100.0	100.0	100.0	00.
Score	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21
Result No.	1	7	6	4	'n	9	7	80	6	10	11	12	13	14	15	16	17	18	17	20	21	75	23	24	25	26	27	28	29

aquaporin 9 - huma	transforming prote	early switch prote	probable hexosyltr	110			hypothetical prote	early switch prote	hypothetical prote	hypothetical prote	early switch prote	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote
JC5791	S11198	A55473	G69290	C84713	T01017	B96601	T49186	B55473	A96601	AF2464	C55473	S15308	G85877	F91033	T30092
0	N	Н	Н	7	7	N	N	N	N	7	7	~	7	7	N
342	348	355	357	358	367	396	399	417	418	420	426	430	470	470	498
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
21	21	21	21	21	21	21	21	21	21	21	21	21	2.1	12	21
30	31	32	33	34	35	36	3.7	38	3.0	40	41	42	43	4 4	4.5

ALIGNMENTS

RESULT 1 A12955		
cell division topological specificity factor minE [imported] - Agro	.mported] -	Agro
C;Species: Agrobacterium tumefaciens		
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-	text_chang	e 18-

bacterium tumefaciens

Nov-2002

C;Accession: A12955
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellé; Karp, P.; Knomero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.

A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A; Title: The Genome of the NuID:21608550; PMID:11743193
A; Accession: A12955
A; Status: preliminary
A; Molecule: type: DNA
A; Residues: 1-86 < KUR>
A; Cross-references: GB:AE008689; PIDN:AAL44063.1; PID:g17741627; GSPDB:GN00187
A; Experimental source: strain C58 (Dupont)

A;Gene: minE A;Map position: linear chromosome

0; Gaps 0; 100.0%; Score 21; DB 2; Length 86; larity 100.0%; Pred. No. 55; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity

45 SVIAK 49 1 SVIAK 5 ð g

cell division topological specificity factor [imported] - Agrobacterium tumefaciens (stre. C, Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Dates: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002 C; Actes: 22-Oct-2001 #sequence_revision 294: Novel N

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK90142.1; PID:g15160139; GSPDB:GN00170
C;Genetics: A;Gene: AGR_L 3134
A;Map position: linear chromosome

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Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 SVIAK 41
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d99632
hypothetical protein MYPU 1670 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
c;Species: Mycoplasma pulmonis
c;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: 690532
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Ritiler: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                       RESULT 3
T32373
hypotherical protein COIB12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
C;Accession: T32373
R;Scheet, P: Maggi, L.
Submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid COIB12.
A;Reference number: Z21156
A;Accession: T32373
A;Accession: T32373
A;Accession: T3237
A;Reference type: DNA
A;Residues: 1-132 <SCH:>A;Residues: 1-132 <SCH:>A;Residues: 1-132 <SCH:>A;Residues: 1-132 <SCH:>A;Experences: EMBL:AF025458; PIDN:AAB70973.1; GSPDB:GN00020; CESP:COIB12.7
A;Experimental source: strain Bristol N2; clone C01B12
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A;Cross-references: GB:AL445566; PID:g14089580; PIDN:CAC13340.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU 1670
A;Genetic code: SGC3
                                                                  Gaps
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0
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A,Introns: 23/3; 90/2
C,Superfamily: Caenorhabditis elegans hypothetical protein C01B12.7
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                     DB 2; Length 86; 55;
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100.0%; Scor.
100.0%; Pred. No. ...
                                                         5; Conservative
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Matches 5; Conservative
              Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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AF1931 hypothetical protein alr1001 [imported] - Nostoc sp. (strain PCC 7120)

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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AF1331
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Preference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphoribosylglycinamide formyltransferase [imported] - Staphylococcus aureus (strain N
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguct
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguct
M.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; F
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

Lancet 357, 1225-1240, 2001

A;Fitle: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Space Sidn: T15115
R;Bradshaw, H; Devlin, K.
Submitted to the EMBL Data Library, July 1997
R;Deacription: The sequence of C. elegans cosmid ZC132.
A;Reference number: Z18294
A;Accession: T15115
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-194 < BRA>
A;Cross-references: EMBL;AF014939; NID:g2275620; PID:g2275628; PIDN:AAB63931.1; GSPDB:GN(A;Experimental source: strain Bristol N2; clone ZC132
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A;Cross-references: GB:BA000019; PIDN:BAB72958.1; PID:g17130347; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
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A;Experimental source: strain N315
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 21-Jun-2002
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100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0;
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100.0%; Score 21; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0;
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Length 194;

100.0%; Score 21; DB 2; I 100.0%; Pred. No. 1.3e+02; .ive 0; Mismatches 0;

5; Conservative

56 SVÍAK 60

1 SVIAK 5

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Query Match Best Local Similarity Matches 5; Conserv

C,Genetics: A,Gene: CESP:ZC132.9 A,Map position: 5 A,Introns: 135/3; 153/3

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tetk family bacterial regulatory protein (AF232237) [imported] - Agrobacterium tumefacier (Species: Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens (C)species: Agrobacterium tumefaciens (C)species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 (C)Accession: A97665 (C)Accession: A97665 (C)Accession: A97665 (C)Accession: A97665 (C)Accession: A97665 (C)Accession: A97665 (C)Accession: A)Alinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A; Affelerence number: A97359; MUID:21608551; PMID:11743194
hypothetical protein AT4924980 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17, 1999
N; Altie: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A; Reference number: A85001; MUID: 20083488; PMID: 10617198
A; Reference number: A85001; MUID: 20083488; PMID: 10617198
A; Reference number: A85001; Muid: 20083488; PMID: 20617198
A; Residues: 1-203 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F13M23.120 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: T05519
R;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.}
a;Reference number: Z15419
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100.0%; Pred. No. 1.3e+02;
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100.0%; Pred. No. 1.3e+02;
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A,Residues: 1-203 <BEV>
A,Cross-references: EMBL:AL035523
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Matches 5; Conservative
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Matches 5; Conservative
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A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: AT4g24980
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
B;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
J; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D; Jones, L.M.; Kaser, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Feference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein CC0485 [imported] - Caulobacter crescentus
C; Date: Scalobacter crescentus
R; Nierman, W.C.; Peldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
R; Nierman, W.C.; Peldblyum, T.V.; Podson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
D; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-200 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC98581.1; PID:g16409878; GSPDB:GN00177
A;Experimental source: strain EGD-e
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A;Molecule type: DNA
A;Residues: 1-197 <STO>
A;Cross-references: GB:AE005673; NID:g13421662; PIDN:AAK22472.1; GSPDB:GN00148
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Indels

Length 197;

100.0%; Score 21; DB 2; I 100.0%; Pred. No. 1.3e+02;

C,Genetics: A,Gene: CC0485 C,Superfamily: 50S ribosomal protein L25

0; Mismatches

5; Conservative

73 SVIAK 77

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1 SVIAK 5

Query Match Best Local Similarity Matches 5; Conserv

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Indels

Query Match
100.0%; Score 21, DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0;

1 SVIAK 5

Length 200;

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C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Datesion: D84959
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Tille: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A;Reference number: A84930; MUID:20445173; PMID:10993077
                                                                                                                                                                                                                                                    basal-body rod modification protein flgD [imported] - Buchnera sp. (strain APS)
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-236 c9TO>
A,Cross-references: GB:AP000398; GSPDB:GN00144
C,Genetics: A,Genetics: A,Ge
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Best Local Similarity 100.
Matches 5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription regulator, TetR family ameR [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AD2889
R;Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Schence, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
WMBERG
UL1 protein - human herpesvirus 2 (strain HG52)
C;Species: human herpesvirus 2
A;Note: host Homo sapiens (man)
C;Accession: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Jun-2000
C;Accession: JQ1494
R;McGeoch, D.J; Cunningham, C.; McIntyre, G.; Dolan, A.
J. Gen. Virol. 72, 3057-3075, 1991
A;Title: Comparative sequence analysis of the long repeat regions and adjoining parts of the ference number: JQ1494; MUID:92113549; PMID:1662697
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A;Molecule type: DNA
A;Residues: 1-224 <MCG>
A;Cross-references: GB:D10470; DDBJ:D01127; NID:g221791; PIDN:BAA01264.1; PID:g221792
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A'Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A'Reference number: AB2577; MUID:21608550; PMID:11743193
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                                          A;Cross-references: GB:AE007869; PIDN:AAK88274.1; PID:g15157738; GSPDB:GN00169
C;Genetics:
A;Gene: AgR C 4617
A;Map position: circular chromosome
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A;Residues: 1.219 -KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43530.1; PID:g17741041; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: ameR
A;Map position: circular chromosome
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                                                                                                                                                                                                                                                              Query Match 100.0%; Score 21; DB 2; Length 219; Best Local Similarity 100.0%; Pred. No. 1.48+02; Matches 5; Conservative 0; Mismatches 0; Indels
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100.0%; Score 21; DB 1; Length 224;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels
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C;Superfamily: varicella-zoster virus gene 60 protein
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A;Residues: 1-219 <KUR>
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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 12, 2004, 06:12:47; Search time 0.307377 Seconds (without alignments) 847.008 Million cell updates/sec Run on:

US-09-890-463-1 21 1 SVIAK 5 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 Total number of hits satisfying chosen parameters: 141681 segs, 52070155 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	tion	agrobacteri	mycoplasma	methanosarc	methanosarc	haemophilus	staphylococ	staphylococ	synechococc	herpes simp	thermoplasm	thermoplasm	streptomyce	buchnera ap	punta toro	xanthomonas	m dimethyla	mycoplasma	rattus norv	rhodopseudo	neurospora	homo sapien	rickettsia	xenopus lae	homo sapien	rattus norv	homo sapien	thermoanaer	salmonella	ralstonia s	candida alb	saccharomyc	lactobacill	enterococcu
	Description	Q8uax0	Q8evw5	Q8tty3	Cmwd8Q	Q57425	Q99v25	68xu8Ö	Q7u4c6	P28278	Q9hir5	Q97bx1	Q82kf0	P57421	P03516	034260	P75113	P47403	P00774	P81379	P19392	Q8nh53	Q92i78	057383	P06746	P06766	014520	Q8rd88	P26400	Q8y387	093807	003957	Q88x53	Q831n1
SUMMARIES	ŒĨ	MINE AGRIS	RL27 MYCPE	SR19 METAC	SR19 METMA	YA7B HAEIN	PUR3_STAAM	PUR3 STAAW	RNH2_SYNPX	VGLL_HSV2H	RS3 THEAC	RS3_THEVO	RNHZ STRAW	FLGD_BUCAI	VNST_PTPV	EXBB_XANCP		RS3 MYCGE	EL2_RAT	CY1 RHOVI	MATA NEUCR	OYN1 HUMAN	Y542 RICCN		DPOB HUMAN	DPOB RAT	AQP7 HUMAN	MUA1 THETN	RFBX SALTY	SAHH RALSO	TBG CANAL			SYR_ENTFA
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ď	% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	00	8	00	00	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	0	100.0
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Q9ce12 lactococcus P38788 saccharomyc Q40545 nicotiana t P22317 alcaligenes Q11174 caenorhabdi Q08759 xenopus lae O76031 homo sapien Q9jhs4 mus musculu	P06876 mus musculu P46200 bos taurus P10242 homo sapien P01103 gallus gall
SYR_LACLA YHM4_YEAST KPYA_TOBAC HOXF_ALCEU GHIT_CABEL MYB_XBNLA CLPX_HUMAN	MYB_MOUSE MYB_BOVIN MYB_HUMAN MYB_CHICK
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                         Adalagan J.E., Nuchaeum.C., Roy A., Endrizzi M.G., Macdonald P., Ralagan J.E., Nuchaeum.C., Roy A., Endrizzi M.G., Macdonald P., Fizhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Navlor J., Stange-Thomann N., DeArellano K., Ohnson R., Linton L., McKernan K., Talamas J., Tirrell A., Ye W., A. Linton L., McKernan K., Talamas J., Tirrell A., Ye W., A. Hedderich R., Indram-Smith C., Kuettner H.C., Krzycki J.A., Guss A.M., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario B.C., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander B., The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";

"The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";

Genome Res. 12:332-542(2002).

"S RNA and mediates binding of the 54 kDa subunit of the SRP (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBUNIT: Archaeal signal recognition particle consists of a 7S RNA molecule of 300 nucleotides and two protein subunits: SRP54 and SRP19 (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: Belongs to the SRP19 family.
                                                                                                                                                                                                                                       Archaea; Buryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                             28-FEB-2003 (Rel. 41, Last annotation update)
Signal recognition particle 19 kDa protein (SRP19).
                    101 AA
                                                                                                Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C2A / ATCC 35395 / DSM 2834;
MEDLINE-21929760; PubMed=11932238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                             081TY3;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF 00305; -; 1.
InterPro; IPR002778; SRP19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD006609; SRP19; 1.
                                                                                                                                                                                                         Methanosarcina acetivorans.
              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
SEQUENCE 101 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVIAK 83
                                                                                                                                                                                                                                                                                              NCBI_TaxID=2214;
                                                                                                                                                                         SRP19 OR MA0292.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
              SR19 METAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SR19 METMA
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SR19_METWA
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MEDLINE-22354119; PubMed-12466555;
MEDLINE-22354119; PubMed-12466555;
MEDLINE-22354119; PubMed-12466555;
MEDLINE-22354119; PubMed-12466555;
MEDLINE-22354119; PubMed-12466555;
MEDLINE-22354119; PubMed-1246555;
MEDLINE-2354119; PubMed-1246555;
MEDLINE-2235419; PubMed-124655;
MEDLINE-2354114; PubMed-124655;
MEDLINE-2354114; PubMed-124655;
MEDLINE-2354114; PubMed-124655;
MEDLINE-2354114; PubMed-124655;
MEDLINE-2364114; PubMed-124655;
MEDLINE-236455;
MEDLINE-236455;
MEDLINE-23645;
MEDLINE-23645;
MEDLINE-236
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                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                Score 21; DB 1; Length 86; Pred. No. 40;
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                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                        TIGRFAMS; TIGRO1215; minE; 1.
Cell division; Complete proteome.
SEQUENCE 86 AA; 9703 MW; B0E274F6A48D52F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 735D951C94B7A730 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-WAR-2004 (Rel. 43, Last sequence update)
50S ribosomal protein L27.
Mycoplace
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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HAMAP; MF_00539; -; 1.
InterPro; IPR001684; Ribosomal_L27.
Pfan PF01016; Ribosomal_L27; 1.
PRINTS; PR00063; RIBOSOMALL27.
ProDom; PD003114; Ribosomal_L27; 1.
IIGRPAMS; TIGR00062; L27; 1.
PROSITE; PS00831; RIBOSOMAL_L27; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 95 AA; 10464 MW; 735D951C5
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EMBL; AE009254; AAL44063.1; -. EMBL; AE008359; AAK90142.1; -.
                                                                                                                                                                                                                                                                                                             100.0%;
                                                 PIR; A12955; A12955.
PIR; D98327; D98327.
HAWAP; MF 00262; -; 1.
InterPro; IPR005527; MinE.
Pfam; PF03776; MinE; 1.
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
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Best Local Similarity 10v...
5, Conservative
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45 SVIAK 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=28227;
                                                                                                                                                                                                                                                                                                                                                                                                                         1 SVIAK 5
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MYCPE
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Signal recognition particle; RNA-binding; Ribonucleoprotein;
                                                                                          100.0%; Score 21; DB 1; Length 101; 100.0%; Pred. No. 46;
                                                                                                                                       0; Indels
                                             101 AA; 11415 MW; 8DA2E31AAA9594C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                           Q8PWM'),
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Signal recognition particle 19 kDa protein (SRP19).
SRP19 OR MM1557.
                                                                                                                                                                                                                                                                                                                                               101 AA.
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RESULT 3 SR19_METAC

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PUR3_STAAM
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                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        -!- SUBUNIT: Archaeal signal recognition particle consists of a 78 RNA molecule of 300 nucleotides and two protein subunits: SRP54 and SRP19 (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the SRP19 family.
                                                                                           MEDLINE=22120827; PubMed=12125824; Deptemmeter U., Johann A., Hartsch T., Merkl R., Schmitz R.A., Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C., Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S., Bhatescharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P., Fritz H.-J., Gottschalk G., "The genome of Methanosarcina mazei: evidence for lateral gene
                                                                                                                                                                                         transfer between Bacteria and Archaea.";
J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
-!- FUNCTION: Signal-recognition-particle assembly, binds directly to 7S RNA and mediates binding of the 54 kDa subunit of the SRP (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=RG / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Firzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
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Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal recognition particle; RNA-binding; Ribonucleoprotein;
          Archaea; Buryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 21; DB 1; Length 101; 100.0%; Pred. No. 46; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 AA; 11377 MW; 3F9235C41CF68C74 CRC64;
                                                                 FROM N.A. oel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YA7B_HAEIN STANDARD; PRT; 134 AA. 057425; P96338; 01-N0V-1997 (Rel. 35, Created) 01-N0V-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Hypothetical protein H11077.1.
 Methanosarcina mazei (Methanosarcina frisia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE013390; AAM31253.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF_00305; -; 1.
InterPro; IPR002778; SRP19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01922; SRP19; 1.
ProDom; PD006609; SRP19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                         NCBI_TaxID=2209;
                                                                                                                                                                                                                                                 similarity).
                                                                                STRAIN=Goel
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STRANIE MUSO / ATCC 700699, and N315;
STRANIE MUSO / ATCC 700699, and N315;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                             Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lancet 357:1225-1240(2001)
-!- CATALYTIC ACTIVITY: 10-formyltetrahydrofolate + N(1)-(5-phospho-D-ribosyl)glycinamide = tetrahydrofolate + N(2)-formyl-N(1)-(5-phospho-D-ribosyl)glycinamide.
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   Brandon R.C.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R. Frine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                           Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
-!- SIMILARITY: WEAK, TO BACTERIAL PNUC PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phosphoribosylglycinamide formyltransferase (BC 2.1.2.2) (GAR1
transformylase) (57-phosphoribosylglycinamide transformylase).
PURN OR SAV1072 OR SA0924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 21; DB 1; Length 134; 100.0%; Pred. No. 60;
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-!- SUBUNIT: Homodimer (By similarity).
-!- SIMILARITY: TO OTHER GART FROM BACTERIA AND EUKARYOTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; HI1077.1; -.
InterPro; IPR006419; NWN trans PnuC.
Pfam; PF04973; NNN transporter; 1.
TIGREMS; TIGR01528; NWN trans PnuC; 1.
Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70C1620F88D0E6BF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 AA; 14415 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U32788; AAC22744.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 SVIAK 79
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phosphoribosylglycinamide formyltransferase (BC 2.1.2.2) (GART) (GAR transformylase) (5'-phosphoribosylglycinamide transformylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040777; PubMed=12044378;
MEDLINE=22040777; PubMed=12044378;
Nabar T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatan K., Naimi T., Kuroda H., Cui L., "Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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ACT SITE 146 146 BY SIMILARITY.
SEQÜENCE 188 AA; 21153 MW; D034134258D89AEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purine biosynthesis; Transferase; Complete proteome.
ACT SITE 146 BY SIMILARITY
SEQUENCE 188 AA; 21166 MW; F0364618F275FA30 CRC6
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NCBI_TaxID=196620;
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HSSP: P08179; 1GAR.
SWISS-2DPAGE; 099725; STRAN.
Interpro; IPR002376; formyl transf.
PROSITE; PS00373; GARŢ; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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INICETPO: IPR0023776; formyl transf.
Pfam; PF00551; formyl transf; 1...
PROSITE; PS00373; GART; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus (strain MW2).
                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP003361; BAB57234.1; -. EMBL; AP003132; BAB42169.1; -.
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PUR3_STAAW
    SOUND STANKE AND SOUND S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: This enzyme is an endonuclease that degrades the RNA of RNA-DNA hybrids specifically (By similarity).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22825697; PubMed=12917641;
Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P., Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
"The genome of a motile marine Synechococcus.";
Nature 424:1037-1042(2003)
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF 00052; -; 1.
InterPro; IPR001352; RNase HII/HIII.
Pfam; PF01351; RNase HII; 1.
Hydrolase; Nuclease; Endomuclease; Manganese; Complete proteome.
ACT SITE 42 42 BY SIMILARITY.
ACT SITE 138 BY SIMILARITY.
ACT SITE 157 BY SIMILARITY.
SEQUENCE 224 AA; 24310 MW; 7F21360ABC4C54AB CRC64;
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100.0%; Score 21; DB 1; Length 188; 100.0%; Pred. No. 82;
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                                    0; Indels
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BY SIMILARITY.
BY SIMILARITY.
7F21360ABC4C54AB CRC64;
                                                                                                                                                                                                                                                                                                                                      Bacteria; Cyanobacteria; Chroococcales; Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphomonoester.
-!- COFACTOR: Manganese (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Belongs to the RNase HII family.
                                                                                                                                                                                                                             15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ribonuclease HII (EC 3.1.26.4) (RNase HII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                               224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 21; DB 100.0%; Pred. No. 96;
                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                    Synechococcus sp. (strain WH8102)
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                                    5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
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Query Match
Best Local Similarity
                                                                                                       181 SVIAK 185
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       RNHB OR SYNW2144.
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                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=84588;
                                                                      1 SVIAK 5
                                                                                                                                                                                                                                                                                      Ribonuclease HII
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ID VGLL HS
AC P28278;
DT 01-DEC-
DT 01-DEC-
DT 15-MAR-
DE G1ycopx
                                 Matches
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Best Local Similarity
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RS3_THEVO
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    SO THE PRESENTATION OF THE PROPERTY OF THE PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=92113549; bubMed=1662697;
MEDLINE=92113549; bubMed=1662697;
"Comparative sequence analysis of the long repeat regions and adjoining parts of the long unique regions in the genomes of herpes simplex viruses types 1 and 2.";
J. Gen. Virol. 72:3057-3075(1991).
                                                                                                                                                                                                                                                                                                                       Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ASSOCIATED WITH GLYCOPROTEIN H (GH) TO FORM A COMPLEX IMPORTANT FOR INFECTION AND CELL FUSION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the herpesviruses glycoprotein L family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .) (POTENTIAL)
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-!- FUNCTION: Binds the lower part of the 30S subunit head (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21; DB 1; Length 224; Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
GLYCOPROTEIN L.
N-LINKED (GLCNAC. . .) (PC
; CD585849250D7CIF CRC64;
GL OR ULI.

Herpes simplex virus (type 2 / strain HG52).

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FFB-2003 (Rel. 41, Created)
28-FFB-2003 (Rel. 41, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 225 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20479972; PubMed=11029001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D10470; BAA01264.1; -.
EMBL; 286099; CAB66761.1; -.
EMIT; JQ1494; WMBEHG.
InterPro; IPR007923; Herpes_UL1.
Pfam; PF05259; Herpes_UL1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 AA; 25192 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30S ribosomal protein S3P. RPS3P OR TA1265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermoplasma acidophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224
170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 SVIAK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SVIAK 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=DSM 1728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THEAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                           Dolan A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
RS3_THEAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S., Kawashima-Ohya Y., Matanabe K., Yamazaki M., Kanahori K., Kawamoto T., Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.; "Archaeal adaptation to higher temperatures revealed by genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
-!- SUBUNIT: Part of the 30S ribosomal subunit.
-!- SIMILARITY: Belongs to the S3P family of ribosomal proteins.
-!- SIMILARITY: Contains 1 KH type-2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGR01008; rpsC_B_A; 1.
PROSITE; PSSOS13; KH TYPE_2; 1.
PROSITE; PSOSO548; RIEDSOWAL S3; FALSE NEG.
Ribosomal protein; RNA-binding; rRNA-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
-!-SUBUNIT: Part of the 30S ribosomal subunit.
-!- SIMILARITY: Belongs to the S3P family of ribosomal proteins.
-!- SIMILARITY: Contains 1 KH type-2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٠,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 21; DB 1; Length 225; 100.0%; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 225 AA; 24726 MW; FE2B2B220091017F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence of Thermoplasma volcanium.";
Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAÞ; MF_01309; -; 1.
InterPro; IPR004087; KH_dom.
InterPro; IPR009019; KH_prok.
InterPro; IPR004044; KH_TYPE_2.
InterPro; IPR001351; Ribosomal_S3_C.
InterPro; IPR005703; S3_euk_arch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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STRAIN=GSS1 / DSM 4299 / JCM 9571;
MEDLINE=20570466; PubMed=11121031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00013; KH; 1.
Pfam; PF00189; Ribosomal S3 C; 1.
SMART; SM00322; KH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoplasmataceae; Thermoplasma.
NCBI_TaxID=50339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30S ribosomal protein S3P.
RPS3P OR TV0334 OR TVG0336522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL445067; CAC12389.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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BUCAI
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                                                                                                                                                                                                                                                                                                                                                     RESULT 13
FLGD_BUCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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VNST PTPV
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                                 R EMBLI, ALCUSTO, 1.

R HAMAP: NF 01309 - ; 1.

R ILGEPTO; IPR004087; KH dom.

R ILGEPTO; IPR004019; KH prok.

DR ILGEPTO; IPR004044; KH TYPE 2.

DR ILGEPTO; IPR004044; KH TYPE 2.

DR ILGEPTO; IPR004131; Ribosomal 83 C.

DR Pfam; PF00189; Ribosomal 83 C; 1.

DR PAMET; SM00322; KH; 1.

DR PROSTIE; PS50822; KH; 1.

DR PROSTIE; PS50829; KH TYPE 2; 1.

DR PROSTIE; PS50849; KH TYPE 2; 1.

DR PROSTIE; PS00548; RIBOSOMAL 83; FALSE NEG.

MRIBOSOMAL PYPE 2; 1.

DR RIBOSOMAL PYPE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermithis.";
Nat. Biotechnol. 21:526-531(2003).
--- FUNCTION: This enraryme is an endonuclease that degrades the RNA of RNA-DNA hybrids specifically (By similarity).
--- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces avermitilis.
Bacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                    100.0%; Score 21; DB 1; Length 225; 100.0%; Pred. No. 97; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; Pubmed=11572948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFACTOR: Manganese (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: Belongs to the RNase HII family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
16-WAR-2004 (Rel. 43, Last annotation update)
RNHB OR RNH OR SAV2453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 AA
 or send an email to license@isb-sib.ch)
                            EMBL; AP000992; BAB59476.1; -.
                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphomonoester.
                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              SVIAK 96
                                                                                                                                                                                                                                                                                                                                                  1 SVIAK 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAW
                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                  Matches
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 407:81-86(2000).
-!- FUNCTION: REQUIRED FOR FLAGELLAR HOOK FORMATION. MAY ACT AS A SCAFFOLDING PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
                                                                                                                                                         HAMAP; MF 00052; -: 1.
InterPro; IPR001352; RNase HII/HIII.
Pfam; PP01351; RNase HII; I.
Hydrolase; Nuclease; Endonuclease; Manganese; Complete proteome.
ACT_SITE 27 BY SIMILARITY.
ACT_SITE 119 BY SIMILARITY.
ACT_SITE 118 BY SIMILARITY.
SEQUENCE 233 AA; 25206 MW; ADD09E96316IFE19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 21; DB 1; Length 233; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
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InterPro; IPR005648; FlgD.
Pfam; PF03963; FlgD; 1.
Flagellum; Complete proceome.
SEQUENCE 236 AA; 26187 MW; E15EAA2D3D84F293 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequence update)
16-00T-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Basal-body rod modification protein flgb. FLGD OR BU339.
                                                                                                                                 EMBL; AP005030; BAC70164.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 SVIAK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Tokyo 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 SVIAK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchnera sp. APS."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVIAK 5
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Search completed: August 12, 2004, 06:20:04 Job time : 4.30738 secs
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                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=ATCC 33913 / NCPPB 528;
MEDLINE=22022145; PubMed=12024217;
MEDLINE=22022145; PubMed=12024217;
Med Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Alves L.M.C., do Amaral A.M., Bertollini M.C., Camarop L.E.A.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wiggerich H.G., Klauke B., Koeplin R., Priefer U.B., Puehler A.; "Unusual structure of the tonB-exb DNA region of Kanthomonas campestris; py. campestris: tonB, exbB, and exbD1 are essential for ferric iron uptake, but exbD2 is not."; J. Bacteriol. 179:7103-7110(1997).
                                                 16-0CT-2001 (Rel. 40, Last annotation update)
Nonstructural protein NS-S.
Punta toro phlebovirus.
Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xanthomonas campestris (pv. campestris).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
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                                                                                                                                                                                                                                                                                                                                                                PIR; A04108; MNVUPT.
Nonstructural protein; Transcription.
SEQUENCE 250 AA; 29097 MW; 2C8909A1EDAD90D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
  250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                      update)
                                        Last sequence
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  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98037510; PubMed=9371459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xanthomonadaceae; Xanthomonas.
                         (Rel. 01, Created)
(Rel. 01, Last seq
                                                                                                                                                                                                                                                                                                                                                     EMBL; K02736; AAA47115.1; -.
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Best Local Similarity 100...
5, Conservative
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  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 SVIAK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVIAK 5
                                                                                                     NCBI_TaxID=11587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXBB OR XCC0009.
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                         21-JUL-1986
21-JUL-1986
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034260;
  VATE TENV
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A., Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F., Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffil D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P., Comparison of the genomes of two Xanthomonas pathogens with differing the propriet and the set of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 417:459-463(2002).
-!- FUNCTION: Involved in the tonB-dependent energy-dependent
-!- FUNCTION: Involved in the tonB-dependent Example to various receptor-bound substrates. Protects exbb from proteclytic degradation and functionally stabilizes tonB (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *imilarity).
-!- SUBUNIT: The accessory proteins exbB and exbD seem to form a
complex with tonB (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- SIMILARITY: Belongs to the exbB / tolQ family.
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POTENTIAL.
A -> R (IN REF. 1).
90138F91BC714508 CRC64;
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EMBL, AE012094; AAM39328.1; -.
InterPro; IPR002898; Mota_ExbB.
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For S; Conservative
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114 1
253 AA;
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TRANSMEM 39
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(orden) Ample Boad sint

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August 12, 2004, 06:12:47; Search time 1.30123 Seconds (without alignments) 1212.385 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
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sp_human:*
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sp_mammal:*
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1: sp_archea:*
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21
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ro		Description	Q9xt66 canis famil	Q8crl6 staphylococ	Q8evw5 mycoplasma	Q8p4c6 xanthomonas	Q7yub8 aphelenchus	Q922z7 mus musculu	Q8haj2 bacteriopha	Q8c8j3 mus musculu	O17211 caenorhabdi	Q8sc48 stx2 conver	Q8e7b3 streptococc	Q89p48 bradyrhizob	Q8vk36 mycobacteri	Q7u080 mycobacteri	Q9xjq6 bacteriopha	Q8zv15 pyrobaculum
SUMMARIES		ID	99XX60	QSCRL6	QBEVWS	Q8P4C6	Q7YUB8	Q922Z7	Q8HAJ2	Q8C8J3	017211	Q8SC48	Q8E7B3	Q89P48	Q8VK36	Q7U080	90rx60	QBZVL5
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Q8ha15 bacteriopha	Q8exa9 leptospira	Q98r43 mycoplasma				m	The same	Q9p435 ajellomyces	_	Q9p434 ajellomyces	2.1				Q8nx89 staphylococ				Q9aav8 caulobacter	Ω		Q9sw28 arabidopsis	Q8fsil corynebacte		on.	095p04 goniopora t	ಹ	Q69112 herpes sımp
162 9 Q8HA15		16	6	n	175 3 Q9P436	m	3	175 3 09P435	175 3 Q9P437	O E	176 13 P87467	11	181 16 Q8YY51	16	16	191 11 P97753	•	16	16	0	200 16 QBY9M4	10	16	8 2	91 6	1.5	3 2 0	224 12 069112
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17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

### ALIGNMENTS

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PRESULT 1

09XT66

PRELIMINARY; PRT; 63 AA.

AC 09XT66

DAG 09XT66

DAG 09XT66

PRELIMINARY; PRT; 63 AA.

AC 09XT66

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DAG 09XT67

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DAG 01XT67

DAG 01XT67

DAG 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)

DAG 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)

CAMPA 02-NOV-1999 (TrEMBLrel. 12, Last annotation update)

CAMPA 02-NOV-1999 (TrEMBLrel. 12, Last annotation update)

CAMPA 11-NOV-1999 (TrEMBLrel. 12, Last annotation update)

RAG 02-NOV-1999 (TrEMBLRel. 12, Last annotation update)

RAG 02-NOV-1999 (TREMBLREL. 12, Last annotation of an eightfold redundant dog RT annotation and characterization of an eightfold redundant dog RT annotation and characterization of an eightfold redundant dog RT annotation and characterization of an eightfold redundant dog RT annotation and characterization of an eightfold redundant dog RT annotation E.;

RAG 01-NOV-1999 (TREMBL/GenBank/DDBJ databases.

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CAG 01-NOV-1999 (TREMBLREL/GENBANK/DDBJ AAD40574.1; ---

DR RESPITE; PROMOS MYE 1; ---

DR ROSITE; PROMOS MYE 1; ---

DR ROMOS MYE 1; ---

DR ROSITE; PROMOS MYE 1
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Length 95;

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10464 MW; 735D951C94B7A730 CRC64;
                                                                                                                                                                                                                                                        100.0%; Score 21; DB 16; 100.0%; Pred. No. 2.9e+02;
                                                            PROSITE; PS00831; RIBOSOMAL_L27; 1.
               TIGRFAMS; TIGR00062; L27; 1.
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Best Local Similarity luv...
5; Conservative
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                                                                                                               Complete proteome.
SEQUENCE 95 AA;
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"The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
                                                                                                                                                                                                                                                        Gaps
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STRAIR=ATC 12228;
STRAIR Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.,
Submitted (Nov-2005) to the EMBL/GenBank/DDBJ databases.
BMBL; ARO16749; ARO16341.1;
Hypothetical procesin; Complete proteome.
SEQUENCE 75 AA; 8090 MW; 98017C60D9C61D9F CRC64;
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=28227;
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                                                                                                                                        100.0%; Score 21; DB 6; Length 63; 100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, APONGAILS AES. 301.25.3-53.00(2002).

EMBL, APONGAILS BAC4424.1;

GO; GO:0005840; C:intracellular; IEA.

GO; GO:0005840; C:intbosome; IEA.

GO; GO:0007312; F:structural constituent of ribosome; IEA.

GO; GO:0006412; P:protein biosynthesis; IEA.

InterPro; IPR001664; Ribosomal L27.

Pfam; PF01016; Ribosomal L27;

PRODOM; PD000114; Ribosomal L27;

ProDom; PD00114; Ribosomal L27;

ProDom; PD00114; Ribosomal L27;

RODOM; PD00144; Ribosomal L27;

RODOM; PD00144; Ribosomal L27;

RODOM; PD00144; Ribosomal L27;

RODOM; PD00144; RIBOSOM; RI
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                                             7707 MW; D8C86265802F3C9F CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillales; Staphylococcus.NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22354719; PubMed=12466555;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis,
                                                                                      Query Match
Best Local Similarity 100.،
درم 5; Conservative
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Best Local Similarity 10v...
5; Conservative
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63
63 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    19 SVIAK 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 SVIAK 75
                                                                                                                                                                                                                                                                                                                                              1 SVIAK 5
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NON TER
SEQUENCE
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QBCRL6
QBCRL6
AC QBCRL0
DT 01-M
DT 01
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10 08EVW
AC 08EVW
AC 08EVW
DT 01-M
DT 00-M
DT
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RECOURNCE FROM N.A.

RECOURNCE FROM N.A.

RECOURNCE FROM N.A.

RECOURNCE 23913 / NCPPB 528;

RECOURNCE 22022145; PubMed=12024217;

RA MEDIINE=22022145; PubMed=12024217;

RA Glassian A.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciaplina L.P.,

RA Carelli R.M.B., Coutinho L.L., Cursino-Santos J.R., Ciaplina L.P.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

RA Equyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M. Lemos M.V.F.,

RA Equyama A.M., Nishi L.T., Leite R.P., Mayaki C.Y., Moon D.H.,

RA Mattins B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Spinola L.A.F., Tarkita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Spinola L.A.F., Tarkita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Spinola L.A.F., Tarkita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Sctubal J.C., Kitajima J.D.,

RA Sctubal J.C., Kitajima J.E.,

RA Mattir A.S9-463(2002)

RA Sctubal J.C., Kitajima J.E.,

RA MEDI AE012499, Amansorter activity; IEA.

GO; GO:0006205; F:receptor activity; IEA.

GO; GO:0006810; P:transport; IEA.

GO; GO:0006810; P:transport; IEA.

BR InterPro; IPRO02482; LysM.

R Pfam: PEO1476; LysM.
       ٥;
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0
       Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
   · 0
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Indels
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100430; TONB_DEPENDENT_REC_1; 1.
1. protein; Complete proteome.
98 Aa; 10593 MW; 0DB6218EB6AAFA60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein XCC3784.
0; Mismatches
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0;

Gaps

Q7YUB8

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STRAIN=CS7BL/6J; TISSUB=Cerebellum;
MEDILINE=22354683; PubMed=12466851;
The FANTOM CONSORTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                      STRAIN=159;
Mutlesa M., Jofre J.;
Mutlesa M., Jofre J.;
Wariability of shiga converting bacteriophages in B. coli O157:H7
strains of human origin isolated from the same outbreak.";
strains of human origin isolated from the same outbreak.";
Submitted (SRP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF548456; AANS919.1; -
SEQUENCE 126 AA; 14230 MW; B8F1776A0329F55A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical S-adenosyl-L-methionine-dependent methyltransferases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                        100.0%; Score 21; DB 9; Length 126; 100.0%; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                             0; Indels
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126 Aa; 14568 MW; 0AB92E67189578CD CRC64;
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01.JAN-1998 (TrEMBLrel. 05, Last sequence update)
01.JUN-2003 (TrEMBLrel. 24, Last annotation update)
01.BIZ.7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                   126 AA.
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                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                structure containing protein.
4732479N06RIK.
                                                                                                                                                                                                     Ouery Match
Query Match
Best Local Similarity 100.v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
         NCBI_TaxID=210928;
                                                      SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                    1 SVIAK 5
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SEQUENCE 12
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Viruses
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017211
ID 01723
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                                                                                                                            Aphelenchus avenae (Mycophagous nematode).
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Aphelenchoidea;
Aphelenchidae; Aphelenchus.
NCBI_TaxID=70226;
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Browne J.A., Goyal K., Tunnacliffe A., Burnell A.;

Browne J.A., Goyal K., Tunnacliffe A., Burnell A.;

Browne J.A., Goyal K., Tunnacliffe A., Burnell A.;

oxidative stress in the anhydrobictic nematode Aphelehus avenae.";

Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY340999; AAQ20895.1;

SEQUENCE 107 AA; 11614 MW; CB0396A67FEC9C32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 21; DB 5; Length 107; 100.0%; Pred. No. 3.3e+02; tive 0; Mismatches 0; Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006681, AAH06681.1; -.
MGD; MGI:97740; Polb.
GO; GO:0006216; P:anti-apoptosis; IMP.
GO; GO:0008220; P:necrosis; IMP.
InterPro; IPR03383; HHH 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00278; HhH1; 1. —
SEQUENCE 111 AA; 12247 MW; E81BBACDF1A3B44F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to DNA polymerase beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                               01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 AA
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 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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 PRT;
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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100...
Si Conservative
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PRELIMINARY;
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Bacteriophage LC159.
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44 SVIAK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 SVIAK 14
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                                                                                         Glutaredoxin.
GLX-1.
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Q8HAJ2;
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Q922Z7;
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5; Conservative
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Hypothetical protein.
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                                                                                                                   100 SVIAK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=216495;
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                                                            1 SVIAK 5
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Matches
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Q89P48
   Matches
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                  MEDLINE=94150718; PubMed=7906398; Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Wilson R., Ainscough R., Anderson K., Coppey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Jones M., Kershaw J., Kirsten J., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latrellle P., Lidoyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Riken L., Roopra A., Saunders D., Showhkeen R., Smaldon N., Smith A., Somhammer E., Staden R., Sulston J., Thomas K., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; T. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,
Yamasaki S., Takeda Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence of Shiga toxin 2-converting phage isolated from Escherichia coli 0157:H7 Okayama strain and comparison with other Bacherichia coli 0157:H7 Okayama strain and comparison with other Subjat toxin 2-converting phages.";

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AP004402; BAB87967.1; --
GO; GO:0004672; F:receptor activity; IEA.

GO; GO:0006815; F:receptor activity; IEA.

GO; GO:0006810; P:transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
NCBI_TaxID=180816;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The sequence of C. elegans cosmid C01B12.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A2C8BA7465940DF2 CRC64;
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Pred. No. 4.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
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(TrEMBLrel. 21, Last sequ
(TrEMBLrel. 25, Last anno
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Hypothetical protein.
Stx2 converting bacteriophage I.
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100.0%;
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PIR; T32373; T32373.
WormPep; C01B12.7; CE07795.
SEQUENCE 132 AA; 15750 MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scheet P., Maggi L.; "The sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Best Local Similarity
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STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Bristol N2;
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01-JUN-2002
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MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusnick C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek I., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Matanabbe A., Idesawa K., Iriquchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AD005948; BAC48900.1; -.
Complete proteome.
SEQUENCE 141 AA; 14457 MW; 9F10019F39AD214B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of Streptococcus agalactiae, a pathogen causing
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Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                             Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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SEQUENCE 141 AA; 15937 MW; 924D2E86930763F5 CRC64;
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                  (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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  141 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Microbiol. 45:1499-1513 (2002).
EMBL, AL766844; CAD45887.1; -.
SagaList; gbs0242; -.
PRT;
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PRELIMINARY;
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InterPro; IPR004360; Gly_bleo_diox.
Pfam; PP00903; Glyoxalase; 1.
Dioxygenase; Pyrruva.
SEQUENCE 152 AA; 16626 NW; 60864662DC2B343D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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MEDLINE=22709107; PubMed=12788972;
MEDLINE=22709107; PubMed=12788972;
PIGATHER T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Colle S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                   Gaps
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EMBL; AE007009; AAK45627.1; -.
                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
4-hydroxyphenylpyruvate dioxygenase C terminal domain containing
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
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                                                Indels
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Conserved hypothetical protein.
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                      Pred. No. 4.3e+02;
Mismatches 0;
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100.08; F1.
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                                             5; Conservative
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                   Similarity
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[1]
SEQUENCE FROM N.A.
MEDLINE=20092464; PubMed=10628842;
MEDLINE=20092464; PubMed=10628842;
Karch H., Schmidt H., Janetzki-Mittmann C., Scheef J., Kroeger M.;
Shiga toxins even when different are encoded at identical positions in the genomes of related temperate bacteriophages.";
Mol. Gen. Genet. 262:600-607(1999).
EMBL; AJ237660; CAB39993.1; -.
FMN; A1124675BE0F5896 CRC64;
                                                                                                                                      Gaps
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=10743;
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                                                                                          Length 152;
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EMBL; BX248338; CAD94218.1; -. Complete proteome. SEQUENCE 152 AA; 16626 MW; 60E64662DC2B343D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                       100.0%; Score 21; DB 16;
100.0%; Pred. No. 4.6e+02;
ative 0; Mismatches 0;
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                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Best Local Similarity
Matches 5; Conserv
                                                                                       Query Match
Best Local Similarity
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 12, 2004, 06:12:47; Search time 1.89549 Seconds (without alignments) 745.314 Million cell updates/sec

US-09-890-463-1 Perfect score:

1 SVIAK 5 BLOSUM62 Scoring table: Sequence:

1586107 segs, 282547505 residues Searched:

Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
5: geneseqp2002s:*
6: geneseqp2003s:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_29Jan04:* 1: geneseqp1980s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARIES

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- ;	Match	Length	EG	ID	1 1	uc
_	100.0	5	m	AAY97147	Aay97147 E	Pigment p
Н	100.0	5	S	ABB99061		N-termina
_	100.0	10	4	AAG87969	Aag87969 S	Saccharom
	100.0	10	4	AAG87968		Saccharom
_	100.0	13	Ŋ	ABP70008		Colour Fa
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_,	100.0	16	2	ABB99074	Abb99074 N	N-termina
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Н	100.0	17	m	AAY97148		Pigment p
	100.0	18	m	AAY97151	Aay97151 F	Pigment p
_	100.0	25	'n	AAY97152		Pigment p
Н	100.0	20	4	AAB62002		
Н	100.0	73	4	ABG14062		
Н	100.0	73	Ŋ	ABP34419		Human iso
Н	100.0	75	9	ABP77483		N. gonorr
н	100.0	92	4	ABB12172		Human MEC
21	100.0	16	4	ABG16073		Novel hum
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21	100.0	89	m	AAG01464		Human sec
21	100.0	91	4	ABG16071		Novel hum
21	100.0	102	7	AAY29549		Human lun
21	100.0	102	ო	AAB44472	Aab44472 F	Human lun
21	100.0	102	4	AAE13814		Human lun
21	100.0	102	7	ADD66504	Add66504 F	Human lun

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#### ALIGNMENTS

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N-terminal; pigment protein from coral tissue; PPCT; fluorescence;
tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet;
UV filter.
                                         Pigment protein from coral tissue N-terminal peptide 1.
           Æ.
          AAY97147 standard; peptide; 5
                               (first entry)
                               04-DEC-2000
                     AAY97147;
RESULT 1
AAY97147
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Acropora aspera.
Acropora horrida.
Montipora caliculata.
Montipora monasteriata.
Porites murrayensis.
Porites lobata.

WO200046233-A1.

10-AUG-2000.

02-FEB-2000; 2000WO-AU000056. 99AU-00008463 (UNSY ) UNIV SYDNEY. 02-FEB-1999;

Dove S; WPI; 2000-532892/48. Hoegh-Guldberg O,

Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.

Claim 3; Page 42; 49pp; English.

The N-terminal peptides shown in AAY97147-48 are from pigment protein from coral tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-700 nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to follow gene expression in transformed tissues) or general dysetuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters

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AAG87968
ID AAG8
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Comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

con-white light or particle emission. CFMs are useful for producing a

transgenic animal which exhibits a novel colour e.g. sheep with blue or

red coloured fleece. They are useful for producing coloured plant

coloured fleece. They are useful for producing admittional

light for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

upholstery. CFMs are useful in the flower industry, in the development of

new varieties of flowering plants. Other contemplated uses include,

expression markers, general reporter molecules, photon traps, UV sinks or

in sunscreens. CFMs modify visible colour in edible and/or ornamental

cfungal species, and in fruits and vegetables to enhance their

marketability. CFMs embedded in a gel matrix improve image quality in
                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
                                                                          Gaps
                                                                                                                                                                                                                                                                                   Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
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                                                  Length 5;
                                                                        0; Indels
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                                                100.0%; Score 21; DB 3; L
100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                              N-terminal amino acid sequence of a CFM #1.
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                                                                                                                                                                                     ABB99061 standard; peptide; 5 AA.
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Prescott M;
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21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
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                                                                                                                                                                                                                                     (first entry)
                                                                        5; Conservative
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UNIV QUEENSLAND.
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Hoegh-Guldberg IO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-740765/80
                                                Query Match
Best Local Similarity
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                        Sequence 5 AA;
(both claimed)
                                                                                                                                                                                                                                                                                                                                                   Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying complementary peptides by analysis of protein and nucleotide sequence databases, useful in drug design.
     (biomatrix). The first all-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae; complementary peptide; peptide identification;
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situations of distorted light spectra (biomatrix). The first all-prochromophore to be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a
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                                                                                                                                                                                              Length 5;
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                                                                                                                                                                                           100.0%; Score 21; DB 5; I
100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
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                                                                                     colour-facilitating molecule (CFM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG87969 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-SEP-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200142276-A1.
                                                                                                                                            Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-2001
                                                                                                                                                                                                                                                                                                    Н
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG87969;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
AAG87969
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The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
                                                                                                                                                                                                                                                                                                                                                                      Identifying complementary peptides by analysis of protein and nucleotide sequence databases, useful in drug design.
                                                                                              Saccharomyces cerevisiae; complementary peptide; peptide identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colour facilitating molecule, CFM, green fluorescent protein, GFP, chromophore, biomatrix, transgenic animal, colouring agent, flower industry; expression marker, reporter molecule, photon trap;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colour Facilitating molecule (CFM) related sequence #SEQ ID 184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 21; DB 4; Length 10; 100.0%; Pred. No. 25; cive 0; Mismatches 0; Indels
                                                                   Saccharomyces cerevisiae peptide, SEQ ID NO: 2917.
                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 432; 488pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP70008 standard; peptide; 13 AA.
                                                                                                                                                                                                                            13-DEC-2000; 2000WO-GB004773.
                                                                                                                                                                                                                                                       99GB-00029471.
                                                                                                            drug discovery; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                        (first entry)
                                                                                                                                         Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                Heal JR;
                                                                                                                                                                                                                                                                                    (PROT-) PROTEOM LID
                                                                                                                                                                                                                                                                                                                                           WPI; 2001-367863/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UV sink; sunscreen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVIAK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SVIAK 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200270703-A2.
                                                                                                                                                                    WO200142276-A1
                                                                                                                                                                                                                                                       13-DEC-1999;
                                                                                                                                                                                                                                                                                                                Roberts GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-2003
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                                      11-SEP-2001
                                                                                                                                                                                                14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP70008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
           AAG87968;
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The invention relates to an isolated colour-facilitating molecule (CFW) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the ore when visualised by a human ey in the absence of excitation by extraneous when visualised by a human ey in the absence of excitation by extraneous con-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel coloure e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for use include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs embedded in a gel matrix improve image quality in cfungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABPS 928-ABPTO48 represent cFM related amino
                                                                                                                                                                                                                                                                                                             Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid sequences. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 21; DB 5; Length 13; 100.0%; Pred. No. 33; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                          Dove SG;
                                                                                                                                                                                                        Brugliera F, Mason J,
Prescott M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-terminal amino acid sequence of a CFM #13.
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 473; 510pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB99073 standard; peptide; 16 AA
                                                        21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
01-MAR-2002; 2002WO-GB000928
                                     02-MAR-2001; 2001US-0273227P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                     (NUFA-) NUFARM LTD.
(UYQU ) UNIV QUEENSLAND.
(JONE/) JONES E L.
                                                                                                                                                                                                        Jones EL, Karan M,
Hoegh-Guldberg IO,
                                                                                                                                                                                                                                                                        WPI; 2002-740765/80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UV sink; sunscreen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200270703-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                white light.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB99073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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0; Gaps

.. 0

'note= "Xaa is any amino acid except Val"

label= Xaa

Misc-difference

/note= "Xaa is any amino acid except Met"

/label= Xaa

Misc-difference

WO200270703-A2

12-SEP-2002.

'note= "Xaa is any amino acid except Lys"

Location/Qualifiers

label= Xaa

Misc-difference

Key

Unidentified.

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The invention relates to an isolated colour-facilitating molecule (CFW) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous conventies light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for produing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs embedded in a gel matrix improve image quality in contemplations of fistorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
                                                                                                                                                                                                                                                                                                                Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; DB 5; Length 16; 100.0%; Pred. No. 42; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                 Dove SG
                                                                                                                                                                                                                                 Мавоп Ј,
                                                                                                                                                                                                                             Brugliera F,
Prescott M;
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 281; 510pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colour-facilitating molecule (CFM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB99074 standard; peptide; 16 AA.
                                              01-MAR-2002; 2002WO-GB000928,
                                                                               02-MAR-2001; 2001US-0273227P
21-MAR-2001; 2001AU-00003874
15-OCT-2001; 2001US-0329816P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                    (NUFA-) NUFARM LID.
(UYQU ) UNIV QUEENSLAND.
(JONE/) JONES E L.
                                                                                                                                                                                                                               Karan M,
                                                                                                                                                                                                                                                                               WPI; 2002-740765/80
                                                                                                                                                                                                                                            Hoegh-Guldberg IO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SVIAK 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16 AA;
              12-SEP-2002.
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                                                                                                                                                                                                                                                                                                                                                                        white light
                                                                                                                                                                                                                             EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB99074;
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                                                                                                                                                                                                                               Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Dove SG;

Mason J,

Brugliera F,

Karan M,

Jones

Hoegh-Guldberg IO,

02-MAR-2001; 2001US-0273227P. 21-MAR-2001; 2001AU-00003874. 15-OCT-2001; 2001US-0329816P.

(NUFA-) NUFARM LTD. (UYQU ) UNIV QUEENSLAND.

(JONE/) JONES E L.

01-MAR-2002; 2002WO-GB000928

Prescott M;

WPI; 2002-740765/80

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The invention relates to an isolated colour-facilitating molecule (CFW) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human ey in the absence of excitation by extraneous con-white light or particle emission. CFWs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant eversing include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for upholstery. CFMs are useful in the flower inductry, in the development of new varieties of flowering plants. Other contemplated uses include, or expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs embedded in a gel matrix improve image quality in correct contemplated to enhance their marketability. CFMs embedded in a gel matrix improve image quality in current sequence to be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a
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Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colour-facilitating molecule (CFM)
                                                                                                                                                                                                                                        Claim 4; Page 282; 510pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16 AA;
                                                                                                                                              white light
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Best Loca
Matches
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RESULT

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Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; UV sink; sunscreen.

N-terminal amino acid sequence of a CFM #14.

Ŋ

us-09-890-463-1.rag

AAY97148 standard; peptide; 17 AA.

RESULT 9 AAY97148 (first entry

04-DEC-2000

AAY97148;

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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
                                                                                                                                                                          Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brugliera F, Mason J, Dove SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 100.0%; Score 21; DB Local Similarity 100.0%; Pred. No. 42; tes 5; Conservative 0; Mismatches
                                                                                                                                      N-terminal amino acid sequence of a CFM #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colour-facilitating molecule (CFM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 281; 510pp; English.
              ABB99072 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prescott M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002; 2002WO-GB000928.
                                                                                                                                                                                                                                                                                                                                                                                                                                            32-MAR-2001; 2001US-0273227P.
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(UYQU ) UNIV QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Karan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-740765/80
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Hoegh-Guldberg IO,
                                                                                                                                                                                                                                          UV sink; sunscreen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JONES E L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                       40200270703-A2.
                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               white light.
                                                                                             22-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                12-SEP-2002
                                                     ABB99072;
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ABB99072
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The N-terminal peptides shown in AAY97147-48 are from pigment protein from coral tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-700 nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to follow gene expression in transformed tissues) or general dyestuff (all enained). PPCT may also be used in sunscreen formulations or UV filters
                                                                                                                                                                                                                                                                                                                                                                                          Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-terminal, pigment protein from coral tissue, PPCT, fluorescence, tissue marker, fluorescent marker, dyestuff, sunscreen, ultra violet,
                                                                                    N-terminal, pigment protein from coral tissue, PPCT, fluorescence, tissue marker, fluorescent marker, dyestuff, sunscreen, ultra violet,
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                                                         Pigment protein from coral tissue N-terminal peptide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pigment protein from coral tissue N-terminal peptide 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY97151 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 42; 49pp; English.
                                                                                                                                                                                                                                           02-FEB-2000; 2000WO-AU000056.
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                                                                                                                                                                                                                                                                                                                                   Hoegh-Guldberg O, Dove
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-532892/48.
                                                                                                                                                                                                                                                                                                   (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                  Acropora horrida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVIAK 5
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                                                                                                                                                                                WO200046233-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (both claimed)
                                                                                                                                                                                                                                                                        02-FEB-1999;
                                                                                                                                                                                                             10-AUG-2000
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                                                                                                                    UV filter.
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Acropora aspera.

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Gaps

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1 SVIAK 5 SVIAK 5

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Matches

5; Length 16; 0; Indels ; 0

Gaps

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0; Indels

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The N-terminal peptides shown in AAY97151-52 are from pigment protein from coral tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a human Cdc5 (hCdc5) protein. The hCdc5 cDNA is useful in the therapy of pathologies such as diseases, syndromes, or other undesirable conditions resulting from defects in cell cycle progression which may result from hCdc5 gene, in the regulation of the hCdc5 gene or in a step downstream of hCdc5 in the regulation of call cycle progression through Q2 and entry into mitosis. It is useful for treating a patient having a hyperproliferative disease such as cancer, coronary artery disease, pulmonary vascular obstructive disease, and other disorders of ahonomal callular proliferation (see AAB61997 for various used of the hCdc5 gene). The present sequence represents a fragment of the c-myb protein, used for amino-terminal
  capable of emitting
light useful as tissue marker,
                                                                                                                                                                                                                       nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to follow gene expression in transformed tissues) or general dyestuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cdc5; hCdc5 cell cycle progression; hyperproliferative; cancer; human; coronary artery disease; cellular proliferation; cardiac injury; C-myb; myocardial infarction; cytostatic; cardiant; vasotropic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             techniques for treating diseases related to cell cycle defect such as
cancer, coronary artery disease, pulmonary obstructive vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids comprising human Cdc5 gene useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 3; Length 25; 100.0%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
Novel pigment protein derived from corals fluorescence upon irradiation by incident fluorescent marker or general dyestuff.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-myb protein fragment (residues 92-141).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB62002 standard; protein; 50 AA.
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                                                                                          Example 2; Page 18; 49pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SVIAK 5
                                                                                                                                                                                                                                                                                                                                        Sequence 25 AA;
                                                                                                                                                                                                                                                                                            (both claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bernstein HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                           Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal; pigment protein from coral tissue; PPCT; fluorescence;
tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet;
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                                                                                                                                                    02-FEB-2000; 2000WO-AU000056.
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Montipora caliculata.
                                                                                                                                                                                                                                                                                                                               WPI; 2000-532892/48.
                    Porites murrayensis.
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Matches 5; Conserv
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                                                              WO200046233-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   claimed)
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                                                                                                                                                                                             02-FEB-1999;
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Query Match

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Dove S;

Hoegh-Guldberg O,

UV filter.

AAY97152;

RESULT 11

WPI; 2000-532892/48.

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Sequence 73 AA;
                            Query Match
                                                     Matches
                                                                                                                                              RESULT 14
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                                                                                                                                                                                   The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN) primers, ollowers, and for chromosome and gene mapping, and in recombinant production of (II). (II) the polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (I) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations trappositive for assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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0
                                                    Length 50;
                                                 100.0%; Score 21; DB 4; Length 50
100.0%; Pred. No. 1.5e+02;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 44421; 103pp; English.
                                                                                                                                                                                                                                                                           Novel human diagnostic protein #14053.
homology studies with hCdc5 protein
                                                                                                                                                                                                ABG14062 standard; protein; 73 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                  (first entry)
                                                                           5; Conservative
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N-PSDB; AAS78249.
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                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                               26 SVIAK 30
                                                                                                     1 SVIAK 5
                          Sequence 50 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biodiversity.
                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                            Matches
                                                                                                                                                                     RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; dimune modulation; haematopolesis regulation; tissue growth; angiogenesis; activin; inhibin; chemoclactic; chemokinetic; heamostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic, antipsoriatic; antidiabetic; cytostatic; hootropic; neuroprotective; antichatheroselerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antibifiammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
                                                                                       Gaps
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0
100.0%; Score 21; DB 4; Length 73; 100.0%; Pred. No. 2.4e+02;
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human isomerase-like ORF3392 protein, SEQ ID NO:6784.
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                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-106200/14.
N-PSDB; ABN78445.
                                   Best Local Similarity
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                                                                                                                                                                      1 SVIAK 5
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chemokinetic activity, haemostatic activity, thrombolytic activity,
creceptor/ligand, antiinflammatory activity, tumour inhibition activity,
and analymostic activity, and may also be involved in the determination
of bodily characteristics, fertility and behaviour. ORFX proteins,
confer proliferative disorders may be used in the treatment of cancers,
confer proliferative disorders such as psoriasis and benight tumours,
confer proliferative disorders such as epilepsy and Alzheimer's disease,
corpan transplantation, disorders of tissue growth and regeneration,
diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
corgan transplantation, disorders of tissue growth and regeneration,
diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
storage disease, and infectious diseases caused by viral, bacterial,
contranscripts, in the identification and cloning of homologous
contranscripts, in the identification and cloning of produce transgenic animals
which may be useful for studying the function and/or activity of ORFX
contranscripts, and in drug screening.
contranscripts are precific anithodies, which are useful in the
diagnosis, treatment and monitoring of ORFX associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a waccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New protein from Neisseria gonorrheae, useful for the manufacture of a medicament for treating or preventing N. gonorrheae infection.
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Best Local Similarity
Local 5; Conserve
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N-PSDB; ABZ38453.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 73 AA;
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Gaps
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                                                        100.0%; Score 21; DB 6; L 100.0%; Pred. No. 2.4e+02; ative 0; Mismatches 0;
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Job time : 3.89549 secs
molecules of the invention
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                                                      Query Match
Best Local Similarity
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                              Sequence 75 AA;
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August 12, 2004, 06:19:43; Search time 10.5225 Seconds (without alignments) 149.169 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1292805 seqs, 313927144 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 6, Appli	Sequence 14, Appl	Sequence 235707,	Sequence 201620,	Sequence 281604,	Sequence 259733,	Sequence 6784, Ap	Sequence 2542, Ap	Sequence 196, App	Sequence 196, App	Sequence 196, App	Sequence 200366,	Sequence 252896,	Sequence 39108, A	Sequence 4, Appli
	ID	US-09-757-049A-6	US-09-912-962-14	US-10-424-599-235707	US-10-437-963-201620	US-10-424-599-281604	US-10-424-599-259733	US-09-864-408A-6784	US-10-276-774-2542	US-09-738-973-196	US-09-854-133-196	US-10-144-649A-196	US-10-424-599-200366	US-10-424-599-252896	US-10-425-114-39108	US-09-892-398-4
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	Query Match Length DB	50	52	55	63	99	72	73	16	102	102	102	107	138	142	156
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21
	Result No.	1	7	m	4	Ŋ	9	7	<b>6</b> 0	თ	10	11	12	13	14	15

	Sequence 72020, A Sequence 72011, A Sequence 209489, Sequence 2990, Ap Sequence 252176, Sequence 21085, A		Sequence 7284, A Sequence 7284, A Sequence 121, App Sequence 121, App Sequence 6, Appli Sequence 6, Appli Sequence 945, App Sequence 945, App
10-832-398 10-424-599 10-424-599 10-369-493 10-437-963 10-424-599 10-425-114	4 4 5 6 6 4	US-10-156-275-88 US-09-935-338-105 US-10-380-430-9 US-10-282-122A-64121 US-10-282-122A-63475 US-10-287-226-374 US-10-425-114-53397	10.425-114-728 10.864-761-34819 30-864-761-34819 30-886-251-121 00-844-861A-6 10.343-650A-206 10.017-161-942
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### ALIGNMENTS

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US-09-757-049-6

Sequence 6, Application US/09757049A

Sequence 6. Application US/09757049A

Sequence 6. Application US/09757049A

SEQUENCE 6. Application US/09757049A

SEQUENCE 7. TITLE OF INVENTION METHODS AND COMPOSITIONS FOR REGULATING CELL CYCLE TITLE OF INVENTION METHODS AND COMPOSITIONS FOR REGULATING CELL CYCLE FILE REPERBNCE: UCSF-020/020A

FILE OF INVENTION WIMBER: US/09/757,049A

CURRENT APPLICATION NUMBER: US/09/757,049A

CURRENT APPLICATION NUMBER: US/09/156,316

PRIOR APPLICATION NUMBER: US/09/156,316

PRIOR APPLICATION NUMBER: 1997-09-22

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PARCH NOS: 50
```

2

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APPLICANT: Barbazuk, Bard
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 201620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 281604
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_96309C.1.pep
US-10-424-599-281604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_96978C.1.pep
US-10-437-963-201620
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100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0;
                                          100.0%; Score 21; DB 12; 100.0%; Pred. No. 2.2e+02;
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                                                                                     0; Mismatches
                                                                                                                                                                                                                                                          US-10-437-963-201620
; Sequence 201620, Application US/10437963
; Publication No. US20040123343A1
; GEBRRAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukhary, Andrey A.
APPLICANT: Boukhary, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 281604, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100..
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Best Local Similarity luv...
5, Conservative
                                                                                     Conservative
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ORGANISM: Glycine max
                    Query Match
Best Local Similarity
                                                                                                                                                                           25 SVIAK 29
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US-10-424-599-281604
  US-10-424-599-235707
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: APPLICANT: AND YIHUA
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRESENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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0
                               Smogorzewska, Agata
SINGORZEWSKA, AGATA
TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND
DIAGNOSTIC AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                        ZIP: OCHOUTER READABLE FORM:

MEDIUUTER READABLE FORM:

COMPUTER: IDM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/912,962
FILING DATE: 25-Jul-2001
CLASSIFICATION NUMBER: 09/018,635
FILING DATE: 04-FEB-1998
ATTORNAY/AGENT INFORMATION:
NAME: DATE OF A - FEB-1998
ATTORNAY/AGENT INFORMATION:
NAME: DATE OF A - FEB-1998
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFERAX: 201-487-5800
TELEFERAX: 201-487-580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 21; DB 9; I
100.0%; Pred. No. 2.1e+02;
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                           STREET: 411 Hackensack Avenue
                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
                        Broccoli, Dominique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 52 amino acids TYPE: amino acid
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APPLICANT: de Lange, Titia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                    STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                               CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 133521
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Sequence 2542, Application US/10276774

Publication No. US20040053245A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE REPRENCE: 21272-010

TITLE REPRENCE: 21272-010

CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT PELICATION NUMBER: US/560,875

PRIOR APPLICATION NUMBER: 09/456,914

PRIOR APPLICATION NUMBER: 09/456,914

PRIOR PILING DATE: 2000-04-27

PRIOR PILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SOSTWARE: Custom
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APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NORME/KEY: misc_feature
LOCATION: (1)...(76)
OTHER INFORMATION: Xaa = any amino acid or nothing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 21; DB 12; 100.0%; Pred. No. 3.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 196, Application US/09738973
Patent No. US20020110563A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Algate, Paul A.
APPLICANT: Secrist, Heather
APPLICANT: Indirias, Carol Yoseph
APPLICANT: Benson, Darin R.
APPLICANT: Elliot, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
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Best Local Similarity luv..
S, Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 SVIAK 48
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                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2542
LENGTH: 76
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APPLICANT:
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Publication No. US20040009474A1
Publication No. US20040009474A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20040009474A1e1 Human Polynucleotides and Polypeptides Enco CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT APPLICATION NUMBER: 60/206,690
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR PILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE PASSED for Windows Version 4.0
IENGTH: 73
LENGTH: 73
                                                                                                                                                  Sequence 29733, Application US/10424599
Sequence 29733, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION:
Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION:
Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EENGEN 259733
LENGTH: 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 21; DB 12; Length 72; 100.0%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT3847_76564C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                57 SVIAK 61
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                    SVIAK 5
                                                                                                                           RESULT 6
US-10-424-599-259733
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US-09-864-408A-6784
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Matches

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FEATURE:

RESULT 8

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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; PILE REFERENCE: 38-21(53223)B
; CURRENT FALING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 200366
LED IN O 200366
LET HAVE THE TABLE OF THE TABLE OF
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Shou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: 18-21(53223)B
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 252896
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Sequence 3108, Application US/10425114

PUDIJICATION No. US20040034888A1

SERERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Care Control of the Control of 
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US-10-424-599-200366
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_70391C.1.pep
US-10-424-599-252896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 21; DB 12;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (1)..(107)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Glycine max
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Best Local Similarity
5; Conserve
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                                                                                                                                                                                                                                                                                                                                                   Sequence 196, Application US/09854133
Sequence 196, Application WS/09854133
PUblication No. US20020183499A1
SEQUENCAL INCRMATION:
APPLICANT: Lodges, Michael J.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT PILLING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 7355
SOFTWARE: FastSEQ for Windows Version 3.0
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Publication No. US20030118599A1
GENERAL INPORMATION:
APPLICANT: Lodge, Michael J.
APPLICANT: Fan, Liqun
APPLICANT: Angate, Paul A.
APPLICANT: Angate, Paul A.
APPLICANT: Angate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475c11
CURRENT PELLON NUMBER: US/10/144,649A
CURRENT PELLON NUMBER: US/20-08-21
NUMBER OF SEQ ID NOS: 749
SEQ ID NO 196
LENGTH: 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 21; DB 9; Length 102; 100.0%; Pred. No. 4.38+02; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 200366, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVIAK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVIAK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVIAK 5
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; ORGANISM: Homo
US-10-144-649A-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-854-133-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 196
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Best Local 5
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us-09-890-463-1.rapb

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IED C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRANT APPLICATION DATE: 10,009/892,398
FILING DATE: 27-Jun-2001
CLASSIFICATION = CURROWN>
PRIOR APPLICATION NUMBER: 09/280,590
FILING DATE: CURROWN>
APPLICATION NUMBER: 09/280,590
FILING DATE: CURROWN>
APPLICATION NUMBER: 09/280,590
FILING DATE: CURROWN>
APPLICATION NUMBER: 1340-1-002 N CP2
REFERENCE/DOCKET NUMBER: 26,742
TELECOMMONICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hirai, Hiroshi
Sherr, Charles
Inoue, Kazushi
Badner, Sarah M.
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
THEREOF
                                                                                                                                                                                               ) OTHER INFORMATION: Clone ID: 700208712_FLI.pep
US-10-425-114-39108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 156 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: <UNKnown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Mus musculus
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF EQ ID NOS: 73128
SEQ ID NO 39108
LENGTH: 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09892398
Publication No. US20030028002A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 07601
                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                         41 SVIAK 45
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US-09-892-398-4
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                                                                                                                                                                                   FEATURE:
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                            Gaps
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 100.0%; Score 21; DB 10; Length 156; 100.0%; Pred. No. 6.8e+02;
                            Indels
                            0; Mismatches
Query Match
Best Local Similarity 100.(
Matches 5; Conservative
                                                                             79 SVIAK 83
                                                     1 SVIAK 5
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Search completed: August 12, 2004, 06:51:20 Job time : 10.5225 secs

(010sn) *110/8 @60/s/1/1

us-09-890-463-1.rai

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
               Copyright
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- protein search, using sw model OM protein August 12, 2004, 06:12:47 ; Search time 0.522541 Seconds (without alignments) 493.990 Million cell updates/sec Run on:

US-09-890-463-1 21 1 SVIAK 5

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 389414 seqs, 51625971 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

lssued_patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		* Ouery			SUMMARIES	
No.	Score	Match	Length	DB 	ID	Description
Т	21	100.0	50	m	-09-156	Sequence 6, Appli
7	21	100.0	52	Н	US-08-519-103-14	14
m	21	100.0	52	٣	US-09-018-635-14	Н
4	21	100.0	52	4	- 1	14
Ŋ	21	100.0	81	4	US-09-134-001C-4236	4236
9	21	100.0	102	4		196,
7	21	100.0	111	4	US-09-107-532A-5388	53
œ	21	100.0	156	c	US-08-928-941D-4	4. At
σ	21	100.0	156	m	-08-928-	36
10	21	100.0		4	-09-280-	4
11	21	100.0		4	-09-280	-
12	21	100.0		4	US-09-892-398-4	4
13	21	100.0		4	(A	46
14	21	100.0		4	489-039A-1	
15	21	100.0		4	-09-107	
16	21	100.0		rH	US-08-680-726A-88	
11	21	100.0		٣	60	88,
18	21	100.0		4		
13	21	100.0	332	4	-09-252	2486
20	21	100.0	342	m	US-09-381-810A-1	1, A
21	21	100.0	354	4	3	78
22	21	100.0	401	4	US-09-465-558-70	70. Ap
23	21	100.0	436	4	US-09-543-681A-6760	· G
24	21	100.0	529	4	US-09-323-998E-23	23.
25	21	100.0	529	4	US-09-323-998E-47	47.
26	21	。	529	4	US-09-323-998E-50	Sequence 50, Appl
27	21	100.0	529	4	US-09-323-998E-51	51,

STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Jersey COUNTRY: USA

ZIP: 07601 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible

Sequence 4957, Ap Sequence 11, Appl Sequence 11,		Sequence 16, Appl Sequence 16, Appl Sequence 24, Appl Sequence 24, Appl	
US-09-134-000C-4957 US-09-335-409-11 US-09-568-102-11 US-09-567-969-11 US-09-569-486-11	US-09-568-472-11 US-09-567-899-11 US-09-328-352-7046 US-08-433-522A-16	US-09-135-166-16 US-08-942-046-16 US-09-107-858-24 US-09-579-174-24	US-08-485-455D-71 US-08-482-130C-71 US-08-484-211C-71 US-08-906-769-71
4 10 4 4 4 4	4446	w w w 4	355
598 713 713 713	713 713 1504 32	6 6 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	0000 0000
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### ALIGNMENTS

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        Sequence 6, Application US/09156316
Fatent No. 6183961
GENERAL INFORMATION:
APPLICANT: Bernstein, Harold S.
APPLICANT: Bernstein, Harold S.
TITLE OF INVENTION: Methods and Compositions for Regulating Cell Cycle
TITLE OF INVENTION: Progression
FILE REPERENCE: UCSF-020/01US
CURRENT FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: 60/060,688
EARLIER FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Sequence 14, Application US/08519103

Patent No. 573370

Patent No. 573370

TITLE OF INVENTION:
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSER: KLANBER & JACKSON
                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 21; DB 3; Length 50; 100.0%; Pred. No. 50; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Homo sapiens
US-09-156-316-6
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 SVIAK 30
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US-09-156-316-6
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Gaps
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APPLICANT: de Lange, Titia
Broccoli, Dominique
Smogorzewska, Agata
TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND
DIAGNOSTIC AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: INDEPORTATION
COMPUTER: INDEPORTATION
COMPUTER: INDEPORTATION
COMPUTER: INDEPORTATION
COMPUTER: INDEPORTATION
COMPUTED DATA:
COMPUT
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                                                                              100.0%; Score 21; DB 3; Length 52; 100.0%; Pred. No. 52;
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                                                                                                                                       Indels
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                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   // TOPOLOGY: linear
// MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-912-962-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: ALADDRESSE: KLAUBER & JACKSON
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 4236, Application US/09134001C; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09912962; Patent No. 6586577; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 52 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity luv.v.
F; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                          5; Conservative
MOLECULE TYPE: peptide
                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 SVIAK 31
                                                                                                                                                                                                                                                         27 SVIAK 31
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         ;
US-09-018-635-14
                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-09-912-962-14
                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: de Lange, Titia
APPLICANT: Broccoli, Dominique
APPLICANT: Smogorzewska, Agata
TITLE OF INVENTION: TELOMERE FEREAT BINDING FACTOR AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 21; DB 1; Length 52; 100.0%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/018,635 FILING DATE:
                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/519,103 FILING DATE: Z5-AUG-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILLING DEALLY
CLASSIFICATION:
ATTORNEY/AGENT INPORMATION:
NAME: David A. Jackson
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-142 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPRAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon B.
REGISTRATION NIWBER: 36,113
REFERENCE/DOCKET NUMBER: 600-1-142
TELECHOWINIATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09018635
Parent No. 6297356
GENERAL INFORMATION:
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CARRESPONDENCE ADDRESS: ALAUBER & JACKSON
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 1-
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 52 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-519-103-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 SVIAK 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-018-635-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hirai, Hiroshi
APPLICANT: Sherr, Charles
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
TITLE OF INVENTION: THREOF
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: 412 Hackensack
CITY: Hackensack
STATE: New Jersey
ZIATE: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,941D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; DB 4; I 100.0%; Pred. No. 1.1e+02;
                                                                                                                                             SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...111
SEQUENCE DESCRIPTION: SEQ ID NO: 5388:
US-09-107-532A-5388
                                                                                                                                                                                                                                                                                                                                                NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecium
                                                                                   MEDIUM TYPE: CD/ROM ISO9660
                                                                                                        COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08928941D Patent No. 6180763 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5388:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 SVIAK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SVIAK 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-928-941D-4
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            APPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPERMINES FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PAPLICATION NUMBER: US 60/064,964
PRIOR PAPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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0
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APPLICANT: Modamath, Roadoh
APPLICANT: Mohamath, Roadoh
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 196
LENGTH: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 21; DB 4; Length 102; 100.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 21; DB 4; Length 81; 100.0%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 196, Application US/09370838
Patent No. 6444425
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
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GENERAL INFORMATION:
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ORGANISM: 1
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100.0%; Score 21; DB 3; Length 156; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels
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ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sherr, Charles
Inoue, Kazushi
Bodner, Sarah M.
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:

NAME: Jackson Esg., David A.

REGISTRATION INBERS: 26,742

REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEPHONE: 201-487-5800

TELEPHONE: 301-487-5800

TELEPHONE: 201-487-5800

TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; DB 4; I 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/280,590A
FILING DATE: 29-Mar-1999
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-280-590A-4
                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09280590A
; Patent No. 6303772
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hirai, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 46
                  Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                Query Match
Best Local Similarity luv...
Si Conservative
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Best Local Similarity
Matches 5; Conserv
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ORIGINAL SOURCE:
                    ;
ORGANISM:
US-08-928-941D-36
                                                                                                                                                                                                                                                                                                             US-09-280-590A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-08-928-941D-36
Sequence 36, Application US/08928941D
Factor No. 6180763
GENERAL INFORMATION:
APPLICANT: Hirai, Hiroshi
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE PATENTIN STATEM:
SOFTWARE PATENTIN BELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,941D
FILING DATE:
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISCHATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CIP
TELEPOMNICATION INFORMATION:
TELEPOMNICATION INFORMATION:
TELEPOMNICATION 11900RAFION:
TELEPOMNICATION 1201-487-5800
TELEPAX: 201-343-1684
                ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-343-1684
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 156 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                       LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                              internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
HYPOTHETICAL: YES
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                       CORRESTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/892,398
FILING DATE: 27-Jun-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION: «Unknown»
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/280,590
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2

REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2

TELEPHONE: 201-487-5800

TELEPHAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 156 amino acide

TYPE: amino acid

STRANDEDNESS: <UNKNOWN>

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FRACHETICAL: NO

FRACHETICA
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Patent No. 6673902
GENERAL INFORMATION:
APPLICANT: Hirai, Hiroshi
                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sherr, Charles
Inoue, Kazushi
                                                                                                                                        ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 46
                                                                            STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
....hes 5; Conservative
                                           CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floor
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                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 21; DB 4; Length 156; 100.0%; Pred. No. 1.6e+02;
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Bodner, Sarah M.
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
                                                                                                                                                                                                                       Bodner, Sarah M.
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE DOCKET NUMBER: 1340-1-002 N CP2
TELECOMMUNICATION INPORMATION:
TELEPRONE: 201-487-5800
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/280,590A
FILING DATE: 29-Mar-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
HYPOTHETICAL: YES
FRAGMENT TYPE: «Unknown»
ORIGINAL SOURCE:
ORGANISM: Gallus gallus
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-280-590A-46
                       Sequence 46, Application US/09280590A
Patent No. 6303772
GENERAL INFORMATION:
APPLICANT: Hirai, Hiroshi
Sherr, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 156 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09892398
Patent No. 6673902
GENERAL INFORMATION:
APPLICANT: Hirai, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                             Inoue, Kazushi
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07601
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US-09-280-590A-46
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1 SVIAK 5
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
LENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FARCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/280,590
FILING DATE: CURKNOWN:

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2
TELECOMMUNICATION INFORMATION:
TELEPAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 21; DB 4; I
100.0%; Pred. No. 1.6e+02;
ilve 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Gallus gallus
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12172, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5886, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
FILING DATE: 27-Jun-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                          LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
FRAGMENT TYPE: «Unknown»
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conserv
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US-09-107-532A-5886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-892-398-46
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                                        ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 4; 100.0%; Pred. No. 2.5e+02;
                                                                                                                                                                                                            COMPUTER: PC
COMPUTER: PC
COMPAGE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
PLING DATE: 30-7un-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: J4 May 1998
APPLICATION NUMBER: 60/051571
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...244; SEQUENCE DESCRIPTION: SEQ ID NO: 5886: US-09-107-532A-5886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GTC-012
TELECOMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: August 12, 2004, 06:21:04 Job time : 1.52254 secs
                                                                                                                                                                                              MEDIUM TYPE: CD/ROM ISO9660
                                                              STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 5886:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
NUMBER OF SEQUENCES: 7310
                                                                                                         STATE: Massachusetts
                                                                                                                                                 ZIP: 02354
COMPUTER READABLE FORM:
                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 5, Conservative
                                                                                       CITY: Waltham
                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 SVIAK 190
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 12, 2004, 06:12:47; Search time 1.56762 Seconds (without alignments) 1043.144 Million cell updates/sec Run on:

US-09-890-463-2 83 1 SVIAKQMTYKVYMSGTV 17 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	protein of short-c	hypothetical prote	delta-(L-alpha-ami	surfactin syntheta		O		sugar transport sy	hypothetical prote	hypothetical prote	microcystin synthe	odorant receptor (	regulatory protein	hypothetical prote	PlsX protein - Aqu	probable leucine d	phosphoserine tran	phosphoserine amin	cal r	probable membrane	hypothetical prote		•-	probable lipoprote	probable lipoprote	probable polymeras	lipoprotein vaig p	probable polymeras	pertussis toxin ch
SUMMAKIES	Ω	G96956	T43498	A40889	I40486	I40485	E86687	C97225	F83890	G83962	T10634	AH2136	A40745	S64488	A70233	G70394	H71473	F81816	H81059	T29945	AG0182	S59262	YGCEVC	A69445	A10383	AH0557	D85540	B64773	H90689	E25973
	DB	5	Ŋ	7	0	C)	7	N	N	ď	N	(1	C)	Ŋ	Ŋ	7	N	7	7	~	7	~	Н	N	7	~1	7	7	7	7
	Length	398	424	3770	3587	3588	218	263	285	294	870	1086	161	170	277	337	346	368	368	459	786	846	3712	140	192	192	226	226	226	227
*	Query Match	4.	51.8	51.8	49.4				•	48.2			47.0			47.0		٠.	•	•		47.0				45.8		45.8	45.8	45.8
	Score	45	43	43	41	41	40	40	40	40	40	40	39	39	39	39	39	39	39	39	39	39	39	38	38	38	38	38	38	38
	Result No.		7	3	4	ഹ	φ	7	œ	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

probable membrane-	protochlorophyllid	thymidine kinase (	exo-alpha-1,4-gluc	probable serine/th	topoisomerase IV c	pertussis toxin ch	Leucine dehydrogen	leucine dehydrogen	probable serine/th	UDP-N-acety1muramo	UMP synthase - sli	hypothetical prote	protochlorophyllid	coiled coil protei	peptide synthetase
F95952	B36716	KIBEMV	H70011	538035	\$73358	F25973	E86605	F72020	G81436	F84955	503826	B86899	S10176	T41515	140457
7	7	Н	7	7	7	н	7	7	7	7	T	7	7	7	Н
234	304	353	554	260	635	227	351	351	384	440	478	552	563	1184	2560
æ	45.8	45.8	45.8	45.8	45.8	44.6	44.6	44.6	44.6	44.6	44.6	44.6	44.6	44.6	44.6
45							_	7	37	37	7	7	7	7	_
38 45	38	38	38	38	38	37	37	37	æ	m	37	m	37	'n	w,

# ALIGNMENTS

RESULT 1 G96956	protein of short-chain alcohol dehydrogenase family [imported] - Clostridium acetobutylic C,Species: Clostridium acetobutylicum	C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C;Accession: G96956	R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, .; Daly, M.J.; Bennett, G.N.; Koonin. B.V.; Smith. D.R.	J. Bacteriol. 183, 4823-4838, 2001	A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A. Peference number. 206000. WITH, 2126025. DMTh, 3126020.	A; Accession: 69656	A; Status: preliminary	A;Molecule type: DNA	A)Cross-references: GB:AE001437; PIDN:AAK78442.1; PID:q15023320; GSPDB:GN00168	A;Experimental source: Clostridium acetobutylicum ATCC824	Cidentics:	Ajdene: CACU462	C,Superfamily: Xylella fastidiosa hypothetical protein XF1835	Query Match 54.2%; Score 45; DB 2; Length 398; Best Local Similarity 47.1%; Pred. No. 3.2; Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;	1 SVIAKQMTYKVYMSGTV 17		
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0

Gaps 0:

Query Match 51.8%; Score 43; DB 2; Length 424; Best Local Similarity 43.8%; Pred. No. 7.8; Matches 7; Conservative 5; Mismatches 4; Indels

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kecter, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Aluthors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucelly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Roch, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scanlon, A; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Vohiyama, T.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Yasumoto, K.; Yata, K.; Yoshida, K.; A; Hitle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Recession: C69718
A; Residues: L-3587 ckun.
A; Residues: L-3587 ckun.
A; Cross-references: CB:29105; CB:AL009126; NID:g26322457; PIDN:CAB12143.1; PID:g2632635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-22, F', 34-41, G', 43-109, D', 111-114, G', 116-138, 'V', 140-258, 'W', 260-308, 'A
A; Residues: 1-22, F', 1917-213, SEL', 2142, 'DSLN', 2146-2444, 'Q', 2446-2712, 'H', 2714-2722, 'H', 272
A; Cross-references: BMBL: X7.2672; NID:9516358; PIDN: CAA51223.1; PID:9516360
R; Fuma, S.; Fujishima, Y.; Corbell, N.; D'Souza, C.; Nakano, M.M.; Zuber, P.; Yamane, K.
Nucleic Acids Res. 21, 33-97, 1993
A; Title: Nucleotide sequence of 5' portion of srfa that contains the region required for A; Reference number: S35517; MUID:93181186; PMID:8441623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: strain 168 trpC2
R;Borchert, S.; Patil, S.S.; Marahiel, M.A.
FBMS Microbiol. Lett. 92, 175-180, 1992
A;Title: Identification of putative multifunctional peptide synthetase genes using highl A;Reference number: S25658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 168, °C', 170-171, 281-283;514-595, 597-647, °R', 649-679, °ETL', 683-693, °DKR', 697,
A;Cross-references: EMBL:X65835; NID:g40202; PIDN:CAA46678.1; PID:g40203
A;Experimental source: strain ATCC 2133,
C;Comment: This protein contains several amino acid-activating domains for the synthesis
the amino-terminal region of this protein, appear to be required for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: srfAB; srfA2
C;Superfamily: surfactin synthetase; acetate-CoA ligase homology; acyl carrier protein h C;Superfamily: surfactin synthesis; carrier protein; duplication; ligase; phosphopantet C;Keywords: antibiotic biosynthesis; carrier protein; duplication; ligase; phosphopantet F;S11-951/Domain: acetate-CoA ligase homology <ACLI>F;968-1035/Domain: acyl carrier protein homology <ACLI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               surfactin synthetase component I - Bacillus subtilis
N;Alternate names: competence protein srfAA; surfactin production protein srfAA; surfact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Experimental source: strain 168
R:Fabret, C.; Quentin, Y.; Guiseppi, A.; Busuttil, J.; Haiech, J.; Denizot, F.
submitted to the EMBL Data Library, March 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;2591-3024/Domain: acetate-CoA ligase homology <ACL3>
F;3041-3108/Domain: acyl carrier protein homology <ACP3>
F;999,2045,3073/Binding site: phosphopantetheine (Ser) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 2; Length 350
Pred. No. 1.66+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Cross-references: EMBL:D13262; NID:9216345; PID:9216347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1036-1481/Domain: repeat <RPT1>F;1542-1995/Domain: acetate-CoA ligase homology <ACL2>F;2013-2081/Domain: acyl carrier protein homology <ACP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: significant sequence differences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :| |: : | :| || 2702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 43.8
Matches 7; Conservative
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Accession: S35518
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NiAlternate names: surfactin synthetase srfA2; surfactin synthetase/competence protein 8

NiAlternate names: surfactin synthetase srfA2; surfactin synthetase component NiAlternate names: surfactin synthetase srfA2; surfactin synthetase surfactin synthetase (BC 6.3.2.-)

C.Species: Bacillus subtilis

C.Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 03-Nov-2000

C.Accession: 140466 $60966; G59718; $46968; $35518; $25658; $34966

R.Cosmina, P.; Rodriguez, F.; de Ferra, F.; Grandi, G.; Perego, M.; Venema, G.; van Sind Mol. Microbiol. 8, 821-831 1993

A.Accession: 1404685; MUD1:93360813; PMID:355609

A.Accession: 1404685; MUD1:9336480; PIDN:CAA49817.1; PID:9396482

A.Accession: 140486 # F.; Gordale type: DNA

A.Residues: 1-3587 <RESS

A.Cross-references: BEMBL:X70356; NID:9396480; PIDN:CAA49817.1; PID:9396482

A.Steperimental source: strain W168 derivative of JH642

A.Accession: Sebuls, H.; Jorgbloed, J.; Venema, G.; van Sinderen, D.

Mol. Microbiol. 15, 55-63, 1995

A.Title: A small gene, designated coms, located within the coding region of the fourth a A.Residues: 977-1104 <AHAM>
A.Residues: 977-1104 <AHAM>
A.Residues: 977-1104 <AHAM>
A.Residues: 977-1104 <AHAM>
A.Residues: 907-1104 <AHAM>
A.; Brusch, S.; Bruschi, C.V.; Caldwell, B.; Caphano, V.; Carter, N.; C.; Bruschi, S. D.; Errington, J.; Funa, S.; Galizzi, A.; Gallen

A.; Bhlich, S. D.; Erritz, C.; Pujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen

A.; Authors: Poulger, D.; Fritz, C.; Pujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
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Livay.

Livay.

A,Reference number: A40889; MUID:91286299; PMID:2061333

A,Recession: A40889

A,Roccession: A40889

A,Roccession: A40889

A,Rosidues: 1-3770 «MAC>

A,Residues: 1-3770 «MAC>

A,Cross-references: GB:X54853; NID:92318; PIDN:CAA38631.1; PID:92319

A,Rote: the sequence of residues 3129-3148 and the corresponding nucleotide sequence are A,Genetics:
A,Genetics:
A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetic
                                                                                                                                                                                                                                                                                                                                            A40889

A6089

A6089

A6089

A61A-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase - Emericella nidulans
N;Alternate names: ACV synthetase
C;Species: Emericella nidulans, Aspergillus nidulans
C;Species: T-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 03-Nov-2000
C;Accession: A40889; S16466
R;MacCabe, A.P.; van Liempt, H.; Palissa, H.; Unkles, S.E.; Riach, M.B.R.; Pfeifer, E.;
A;Title: delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase from Aspergillus nithway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
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                                                                                                |::| :|| :|| SIVALNKSYEVYFTGT 16
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Best Local Similarity 50.0
Matches 8; Conservative
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                                                                                                                     DP
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A;Status: translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Accession: 140485

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C;Accession: B86687
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Benome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssr A;Reference number: A86625; WUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein CAC2643 [imported] - Clostridium acetobutylicum C;Species: CP3201 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: C97225 R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. A;Title: Senome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clost A;Reference number: A96900; MUID:21359325; PMID:21359325
               C;Keywords: antibiotic biosynthesis; carrier protein; phosphopantetheine; phosphoprotein $550-956,Domain: acetate-CoA ligase homology <ACL1>
F;974-1042/Domain: acetatrier protein homology <ACP1>
F;91043-1488/Domain: repeat <RP71>
                                                                                                                                                                                                                                                                    F;2589-3025/Domain: acetate-CoA ligase homology <ACL3>
F;3042-3109/Domain: acyl carrier protein homology <ACP3>
F;1006,2043,3074/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE001437; PIDN:AAK80590.1; PID:g15025670; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                           F;1549-1993/Domain: acetate-CoA ligase homology <ACL2>F;2011-2079/Domain: acyl carrier protein homology <ACP2>
                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
49.4%; Score 41; DB 2; Les
Best Local Similarity 43.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 4; Mismatches 5;
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14;
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17;
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Pred. No.
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Best Local Similarity
7, Conserve
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Best Local Similarity
7; Conserve
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A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rykunst, F.; ogsawars, N.; Alberten, M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. A.; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, dect, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumono, M.; Kurita, K.; Lapidus, A.; Latdinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Sanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, A.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Tanako, V.; Uchiyama, A.; Heference number: Ag9580; MulD:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Cross-references: EMBL:D13262; NID:g216345; PID:g216346
A; Cross-references: EMBL:D13262; NID:g216345; PID:g216346
A; Cross-references: EMBL:D13262; NID:g216345; PID:g216346
A; Note: protein sequence not complete, the nucleotide sequence was submitted to the EMBI
B; Nakano, M.M.; Magnuson, R.; Myers, A.; Curry, J.; Grossman, A.D.; Zuber, P.
A; Title: srfa is an operon required for surfactin production, competence development, an A; Reference number: A37323; MUID:91154134; PMID:1847909
C;Species: Bacillus subtilis
C;Date: 12-Aug-1996 #text change 03-Nov-2000
C;Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text change 03-Nov-2000
C;Accession: 140485; B69718; S35517; A37323; S46867; A43705; S34985
R;Cosmina, P.; Rodriguez, F.; de Ferra, F.; Grandi, G.; Perego, M.; Venema, G.; van Sind Mol. Microbiol. B, 821-831, 1993
A;Title: Sequence and analysis of the genetic locus responsible for surfactin synthesis A;Reference number: 140485; MUID:99360813; PMID:8955609
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R, Funa, S.; Fujishima, Y.; Corbell, N.; D'Souza, C.; Nakano, M.M.; Zuber, P.; Yamane, K. Nucleic Acids Res. 21, 33-97, 1993
A;Title: Nucleotide sequence of 5' portion of srfA that contains the region required for A;Reference number: S35517; MUID:93181186; PMID:8441623
A;Recession: S35517
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A; Cross-references: EMBL:X72652, NID:9516358; PIDN:CAA51222.1; PID:9516359
A; Experimental source: strain 168 trpC2
C; Comment: This enzyme is one of several in the multienzyme complex that synthesizes the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Nakano, M.M.; Xia, L.; Zuber, P. J. Bacteriol. 173, 5487-5493, 1991
A;Title: Transcription initiation region of the srfA operon, which is controlled by the A;Reference number: A43705; MUID:91358326; PMID:1715856
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A;Cross-references: GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB12142.1; PID:g2632634
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A;Cross-references: GB:M59939; NID:g14366
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R;Fabret, C.; Quentin, Y.; Guiseppi, A.; Busuttil, J.; Haiech, J.; Denizot,
submitted to the EMBL Data Library, March 1993
                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-3588 <RES>
A;Cross-references: EMBL:X70356; NID:g396480; PIDN:CAA49816.1; PID:g396481
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1 SVIAKQMTYKVYMSGT 16
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A;Gene: srfAA; srfA1
A;Note: srfAA is the first gene of the srfA operon
C;Superfamily: surfactin synthetase; acetate-CoA ligase homology; acyl carrier protein H
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A; Reference number: S46967

A; Molecule type: DNA

A;Accession: S46967

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610 VTPEQLTYLIYTSGS 624
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Best Local Similarity
-has 8; Conserve
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A; Residues: 1-870 <BEV>
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CiSpecies: Bacillus halodurans
CiAccession: G83962
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83962
A;Accessio
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                                                                                                                                                                                                                                                                                                                                                                       Sugar transport system (permease) BH1926 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans (cjate: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: F83890 K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132 A;Accession: F83890 A
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46.2%; Pred. No. 19;
tive 5; Mismatches 2; Indels
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C, Genetics:
C, Gene: BH1926
C, Superfamily: maltose transport protein malG
      48.2%;
ilarity 61.5%;
Conservative
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133 EQLGYKVYLTSTI 145
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les 8; Conserv
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S B, 205-213, 2001
A)MA Res. 8, 205-213, 2001
A)Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A,Reference number: AB1807; MUJD:21595285; PMID:11799840
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C;Keywords: carrier protein; phosphopantetheine; phosphoprotein
F;1015/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
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C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C;Date: 21-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C;Accession: A40745
B;Reseler, K.J.; Sullivan, S.L.; Buck, L.B.
Ccll 73, 597-609, 1993
A;Titles. A zonal organization of odorant receptor gene expression in the olfactory epith A;Reference number: A40745; MUID:9328822; PMID:7683976
A;Accession: A40745
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH2136
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A;Cross-references: GB:BA000019; PIDN:BAB74346.1; PID:g17131740; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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A, Cross-references: GB:L14568; NID:g293757; PIDN:AAA39852.1; PID:g293758
A, Cross-references: GB:L14568; NID:g293757; PIDN:AAA39852.1; PID:g293758
A, Experimental source: olfactory epithalium
A, Note: sequence extracted from NCBI backbone (NCBIP:131747)
C, Superfamily: olfactory receptor OR14
C, Keywords: G protein-coupled receptor; transmembrane protein
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A;Introns: 72/3; 105/3; 257/2; 328/2; 635/1; 685/3; 724/3
C;Superfamily: Arabidopsis thaliana hypothetical protein T13K14.70
A,Cross-references: BMBL:AL080282; GSPDB:GN00062; ATSP:T13K14.80
A,Experimental source: cultivar Columbia; BAC clone T13K14
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C;Species: Mus musculus (house mouse)
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Search completed: August 12, 2004, 06:13:50 Job time : 3.56762 secs
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SVIAKOMTYKVYMSGTV
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26 AKELGYKIYLVG 37
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Best Local Similarity
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A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID: 98065943; PMID: 9403685
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J. Biol. Chem. 269, 21284-21292, 1994
A.Title: Characterization of CBP4, a new gene essential for the expression of ubiquinol-
A.Reference number: A53928; MUID:94342301; PMID:8063753
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A;Experimental source: strain B31
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A;Cross_references: EMBL:Z72959; NID:g1323307; PID:e243557; PID:g1323308; MIPS:YGR174c
A;Experimental source: strain S288C
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                                                                                                                                                                                                            regulatory protein CBP4 precursor - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein G7122; protein YGR174c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 21-Jul-2000
C;Accession: S64488; A53928
R;Hebling, U; Hofmann, B.; Delius, H.
Submitted to the Protein Sequence Database, May 1996
A;Reference number: S64003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein BBG17 - Lyme disease spirochete plasmid G/lp28-2
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-64,'F',66-170 <CRI>
A;Cross-references: GB:U10700; NID:g505645; PIDN:AAA61566.1; PID:g505646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
47.0%; Score 39; DB 2; Length 277;
Best Local Similarity 41.2%; Pred. No. 27;
Matches 7; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Superfamily: Borrelia burgdorferi hypothetical protein BBG17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: mitochondrion; transmembrane protein F;30-51/Domain: transmembrane #status predicted <TVM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: SGD:S0003406; MIPS:YGR174cA;Map position: 7R
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10 AVIAKQRQYKHYL 22
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            3 IAKOMIYKVYMS 14
                                                                     5 ICKPLTYKVIMS 16
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S64488
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Gene: SGD: CBP4
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A;Residues: 1-337 <AQF>
A;Cross-references: GB:AE000723; NID:g2983569; PIDN:AAC07145.1; PID:g2983573; GB:AE00065; A;Cross-references: GB:AE000723; NID:g2983569; PIDN:AAC07145.1; PID:g2983573; GB:AE00065; C;Generics: A;Gene: plsX
A;Gene: plsX
C;Superfamily: phospholipid biosynthesis protein, PlsX type
                                                                                                                                                                  PlsX protein - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 28-Jul-2003
C;Accession: G70394
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
                                                                                                                                                                                                                                                                                                                                                                         Nature 392, 353-358, 1998
Ajtile: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
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98
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Coposin Mode occasin

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 12, 2004, 06:12:47; Search time 1.04508 Seconds (without alignments) 847.008 Million cell updates/sec

US-09-890-463-2 83 1 SVIAKQMTYKVYMSGTV 17 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	D27742 PHERITALIS	bacillus	bacillus		schistoce	_	Sacc	067186 aquifex aeo		neisseria				P36671 escherichia	P26237 rhodobacter		oceanobaci								_	m	7 volvox	vibrio	vibrio	thermon			70612
SUMMARIES	Д	ACVS EMENI	SRF2_BACSU	SRF1 BACSU		SM2A_SCHGR		CBP4 YEAST	PLSX_AQUAE	SERC_NEIMA	SERC NEIMB	SP98_YEAST	ACVS CEPAC	YF62_ARCFU	YAJG_ECOLI	BCHL_RHOCA	KITH HSVMD	MTLD OCEIH	PTK1_YEAST	PARE MYCPN	MURD_BUCAI	CHLB_CHLPT	PYR5_DICDI	CHLB_CHLMO	PPS2_BACSU	YA7B HAEIN			FABA_VIBPA	FABA_VIBVU	KCY THEVO	RHOG HUMAN	BCHL_RHOSH	IL8A_RAT
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P12045 bacillus su Q9Kr69 vibrio chol P43948 haemophilus Q8eu02 oceanobacil Q9zw7 saccharomyc P41606 pinus thunb Q8r0w0 mus musculu P01459 naja haje a P01461 naja haje a Q97bw9 thermoplasm O33877 pseudomonas
PURK BACSU YH74 VIBCH MPL_HAEIN SYE_OCEIH MBIJ_YEAST RPOD_PINTH EPPL_MOUSE CX4_NAJHA CX4_NAJHA CX8_NAJHA CX8_NAJHA SUJI_THEVO
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## ALIGNMENTS

us-09-890-463-2.rsp

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                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zuber P., Yamane K.;
"Nucleotide sequence of 5' portion of srfA that contains the region
required for competence establishment in Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=168;
MEDLINE=97124189; PubMed=8969502;
Yamane K., Kumano M., Kurita K.;
"The 25 degrees-36 degrees region of the Bacillus subtilis
ohromosome: determination of the sequence of a 146 kb segment and
                                                                                                                                                                   PHOSPHOPANTETHEINE (BY SIMILARITY)
PHOSPHOPANTETHEINE (BY SIMILARITY)
PHOSPHOPANTETHEINE (BY SIMILARITY)
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MEDLINE=93360813; PubMed=8355609;
Cosmina P., Rodriguez F., de Ferra F., Grandi G., Perego M.,
Venema G., van Sinderen D.;
                                                                                                         DOMAIN 1 (ADIPATE-ACTIVATING).
DOMAIN 2 (CYSTEINE-ACTIVATING).
DOMAIN 3 (VALINE-ACTIVATING).
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
                                                                                                                                                                                                                            51.8%; Score 43; DB 1; Length 3770; 50.0%; Pred. No. 28; 21ve 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fuma S., Fujishima Y., Corbell N., D'Souza C., Nakano M.M.,
                                                                                                                                                                                               THIOESTERASE (BY SIMILARITY)
422448 MW; CB66B6D232A58CB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1423;
                            Pfam; PF00550; pp-binding; 3.
Pfam; PF00975; Thioesterase; 1.
PRINTS; PR00142; AMPBINDING; BROSITE; PS00142; PROSPHOPANIETHEINE; 3.
PROSITE; PS00455; AMP_BINDING; 3.
PROSITE; PS50075; ACF_DOMAIN; 3.
Ligase; Antibiotic Diosynthesis; Multifunctional enzyme; Repeat; Phosphopantetheine.
                                                                                                                                                            ACYL CARRIER (ACP) 3
                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
15-071-1998 (Rel. 36, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Surfactin synthetase subunit 2.
                                                                                                                                                                                                                                                                                                                                        PRT; 3587 AA
                                                                                                                                                                                                                                                                                                                                                                                                   SRFAB OR SRFA2 OR COML OR BSU03490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 21:93-97(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93181186; PubMed=8441623;
  InterPro, IPR001031; Thioesterase.
Pfam; PF00501; AMP-binding; 3.
Pfam; PF00668; Condensation; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identification of 113 genes.";
Microbiology 142:3047-3056(1996)
                                                                                                                                                                                                                                                                                   |: :||: | | |||
468 SLTSKQLAYVTYTSGT 483
                                                                                                                                                                                                                                                                      1 SVIAKOMTYKVYMSGT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-3077 FROM N.A.
                                                                                                                                                                                                                                                   Conservative
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2002
3087
882
1965
3050
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3078
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1929 200
3020 308
882 108
1965 196
3623 362
3770 AA;
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Matches 8; Conserv
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SEQUENCE FROM N.A.
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         MEDLINE-98044033; PubMed=9384377;

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Kunst F., Ogasawara N., Moszer I., Bolotin A., Borchert S.,

Borriss R., Boursier L., Brans A., Braun M., Briganell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

R. Bronisch F., Devine K.M., Dusterbfet A., Ehrlich S.D., Emmerson P.T.,

R. Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

R. Eritz C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galleron N.,

R. Fritz C., Fujita M., Pujita Y., Molight D., Grandi G.,

R. Allbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

R. Allbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

R. Acuiseppi G., Guy B.J., Haga K., Haicoh J., Harwood C.R., Henaut A.,

Allbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

R. Acuiseppi G., Guy B.J., Lardinois S., Lauber J., Lazarevic V.,

A. Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

R. Kutita K., Lapidus A., Liu H., Masuda S., Kumano M.,

R. Moone D., Pohl T.M., Portetelle D., Porwollik S., Parescott A.M.,

R. Horina N., Perila C., Purnelle B., Roper B., Pose M., Sadaie Y.,

R. Rieger M., Ravolta C., Rocha B., Roche B., Rose M., Sadaie Y.,

Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

R. Scrokin A., Tanakoshi A., Tanaka T., Tarkamaru K.,

R. Takeuchi M., Tamakoshi A., Tanaka T., Tarkamaru K., Yasumoto K., Yata A.,

R. Winters P., Wander A., Yandenbol M., Vanner F., Vassarotti A.,

R. Winters P., Wander C., Yander B., Roch B., Roch B., Roch B.,

R. Woonide R., Wandeler E., Wedler E., Wedler F., Vassarotti A.,

R. Wanters P., Wander C., Yandenbol M., Vanner P., Shin B.S.,

R. Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

R. Rubtils., R. Wander S., Wandenbol M., Vassarotti M.,

R. Subtils., R. Wander S., Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borchert S., Patil S.S., Marahiel M.A., Identification of putative multifunctional peptide synthetase genes using highly conserved oligonucleotide sequences derived from known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLU, ASP AND VAL.
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-!- SIMILARITY: Contains 3 acyl carrier domains.
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EMBL, D50453; BAA08983.1; --
EMBL, Z99105; CAB12143.1; --
EMBL, X65835; CAA46678.1; --
PIR, I40486; I40486.
HSSP, P14687; IAMU.
SUBLILIST, BG10169; SIFAB.
InterPro; IPR000873; AMP-bind.
InterPro; IPR001242; Condensatn.
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MEDLINE=92290255; PubMed=1601288;
MEDLINE=98044033; PubMed=9384377;
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InterPro; IPR006162; Ppantne_S.
Pfam; PP006501; AMP-binding; J
Pfam; PF00668; Condensation; 4.
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R PRINTS; PRO0154; AMPBINDING.
R PRINTS; PRO0154; AMPBINDING.
R PROSITE; PRO0012; PHOSPHOPAINETHEINE; 3.
DR PROSITE; PS00455; AMP BINDING; 3.
DR PROSITE; PS00455; AMP BINDING; 3.
KW Ligrase; Antibictic biosynthesis; Phosphopantetheine; Sporulation; KW Multifunctional enzyme; Repeat; Complete proceome.
FT REPEAT ? 1040 DOMAIN 1 (VAL-ACTIVATING).
FT REPEAT ? 3114 DOMAIN 3 (D-LEU-ACTIVATING).
FT REPEAT ? 3114 ACYL CARRIER (ACP) 1.
CMAIN 970 1036 ACYL CARRIER (ACP) 2.
CMAIN 2015 2082 ACYL CARRIER (ACP) 2.
CMAIN POWAIN POWAIN 2015 2082 ACYL CARRIER (ACP) 3.
CMAIN POWAIN POWAIN ACYL CARRIER (ACP) 3.
CMAIN POWAIN POWAIN ACYL CARRIER (ACP) 2.
CMAIN ACT CARRIER (ACP) 3.
CMAIN ACT CARRIER (ACP) 4.
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A -> V (IN REF. 1).
A -> V (IN REF. 1).
E -> U (IN REF. 1).
ATDLF -> RQICS (IN REF. 1).
TYHQLFEETVQRHKDRPAVIY -> DGCISYSKRLSSATKT
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KL -> NV (IN REF. 1).
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PHOSPHOPANTETHEINE (POTENTIAL)
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RHV -> ETL (IN REF. 1).

EQSIT -> DKRIS (IN REF. 5).

M -> L (IN REF. 5).

PL -> LV (IN REF. 1).
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H -> Q (IN REF. 1).
V -> C (IN REF. 1).
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Q -> D (IN REF. 1).
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A -> V (IN REF. 1).
L -> W (IN REF. 1).
R -> A (IN REF. 1).
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49.4%; Score 41; DB 1; Length 3587;
43.8%; Pred. No. 62;
Live 4; Mismatches 5; Indels
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               Best_Local Similarity 43.8
Matches 7; Conservative
Query Match
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PRT; 3588 AA. 2687 AVTAENLAYMIYTSGT 2702 STANDARD; SRF1_BACSU ID SRF1_BACSU AC P27206; RESULT 3

SEQUENCE OF 1-460 FROM N.A. MEDLINE=91154134; PubMed=1847909;

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RA Kunst E. 20141031; Funned 191843/1; Albertini A.M., Alloni G., RA Kunst E. 20141031; Funned 191843/1; RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Bavedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Ravedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Raberiser L., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., R. Brouillet S., Bruschi C.V., Connerton I.F., Cummings N.J., Daniel R.A., Brain M. S., Deviner K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Raberiach K.D., Errington J., Fabret C., Ferrari E., Foulger D., Raberiach R.D., Galleron N., Gdliseppi G., Guy B.J., Haga K., Haiceh J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kashara Y., Klaerr-Blanchard M., Klein C., Arotis B., Karamata D., Kashara Y., Klaerr-Blanchard M., Klein C., Arotis B., Karamata D., Kashara Y., Klaerr-Blanchard M., Klein C., Arotis B., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Median N., Mellan R., Lapidus R., Lardinois S., Lauber V., Lazarevic V., R. Media N., Mizuno M., Mosetl D., Nakai S., Noback M., Rescan B., Pulic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rescan B., Pulic P., Purnelle B., Rapoport G., Roy M., Sachot B., Rose M., Sachis B., Schleich S., Schroe B., Rose M., Sachot B., Rose M., Sachot B., Rose M., Tacconi E., Takagi T., Takahashi H., Takemaru K., Rasunoto K., Yanamochi M., Tamakoshi A., Tanakoshi A., Tanakoshi A., Tanakoshi A., Tanakoshi A., Tanakoshi A., Tanakoshi M., Vanane K., Vasunoto K., Yata K., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Tosato V., Wambutt R., Wandutt R., Wadler H., Waltzersenegger T., Winters P., Winpat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein B., Toshikawa H.F., Zumstein E., Sohikawa H.F., Zuhikawa H.F., Zuhikawa H.F., Zuhikawa H.F., Zuhikamanoto de the Gram-positive bacterium Bacillus
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STRANT=168 / JH642;
MEDILINE=93860813; PubMed=8355609;
Cosmina P., Rodriguez F., de Ferra F., Grandi G., Perego M.,
Venema G., van Sinderen D.;
"Sequence and analysis of the genetic locus responsible for surfactin synthesis in Bacillus subtilis.";
                                                                                                                                                                                                                                                   MEDLINE 30181186; PubMed=8441623; Fuma S., Fujishima Y., Corbell N., D'Souza C., Nakano M.M., Zuber P., Yamane K.; Wanae K.; Wholeotide sequence 6; portion of srfA that contains the region required for competence establishment in Bacillus subtilis.", Nucleic Acids Res. 21:93-97(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamane K., Kumano M., Kurita K.,
"The 25 degrees-36 degrees region of the Bacillus subtilis
Chromosome: determination of the sequence of a 146 kb segment and
identification of 113 genes.";
Microbiology 142:3047-3056(1996).
                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
01-AUG-1992 (Rel. 23, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                          SRFAA OR SRFA1 OR SRFA OR BSU03480.
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=168; MEDLINE=97124189; PubMed=8969502;
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                                                                      Surfactin synthetase subunit 1
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Best Local Similarity 43.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujishima Y., Yamane K.; "A 10 kb nucleotide sequence at the 5' flanking region (32 degrees) of srfAA of the Bacillus subtilis chromosome."; Microbiology 141:277-279(1995).
                                                                                                                                                                                                                                                                          Subtilis..;
J. Bacteriol. 173:5487-5493 (1991).

J. Bacteriol. 173:5487-5493 (1991).

-!- FUNCTIONAL HIS PROTEIN IS A MULTIFUNCTIONAL ENZYME ABLE TO
ACTIVATE AND POLYMERIZE THE AMINO ACIDS LEU, GLU, ASP AND VAL.
ACTIVATION SITES FOR THESE AA CONSIST OF INDIVIDUAL DOMAINS.
-!- COPACTOR: Contains 3 covalently bound phosphopantetheines.
-!- PATHWAY: Cyclic peptide antibiotic surfactin biosynthesis.
-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                    SEQUENCE OF 1-38 FROM N.A.
MEDIINE-91358326; PubMed-1715856;
MEDARANO M.M., Xia L., Zuber P.;
"Transcription initiation region of the srfA operon, which is controlled by the comP-comA signal transduction system in Bacillus
                  Zuber P.;
"srfA is an operon required for surfactin production, competence
development, and efficient sporulation in Bacillus subtilis.";
J. Bacteriol. 173:1770-1778(1991).
   Nakano M.M., Magnuson R., Myers A.M., Curry J., Grossman A.D.,
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V -> L (IN REF. 1 AND 5)
G -> A (IN REF. 1).
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                                                                                                      STRAIN=168;
MEDLINE=95219080; PubMed=7704255;
                                                                                        SEQUENCE OF 1-64 FROM N.A.
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A -> P (IN REF. 5).

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PT -> GS (IN REF. 1).

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Q -> L (IN REF. 1).

Q -> L (IN REF. 1).

Y -> L (IN REF. 1).
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A -> R (IN REF. 1).

T -> D (IN REF. 1).

A -> R (IN REF. 1).

D -> L (IN REF. 1).

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--- FUNCTION: Unusual circulary permuted GTPase that catalyzes rapid hydrolysis of GTP with a slow catalytic turnover (By similarity).
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STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
MARAMI H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
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Pred. No. 62;
4; Mismatches 5; Indels
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BC02FB157D7F1FDB CRC64;
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
17-MAR-2004 (Rel. 43, Last annotation update)
BNGC OR BH2503.
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           S THE THEFFE THE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUNCTION: ACTS AS CHEWOREPULSIVE GUIDANCE MOLECULE CRITICAL FOR AXON FASCITCULATION AND FOR DETERMINING BOTH THE INITIAL DIRECTION AND SUBSEQUENT PATHFINDING EVENTS OF THE TI AXON PROJECTION.

SUBCELLULAR LOCATION: Secreted (Potential).

TISSUE SPECIFICITY: EXPRESSED IN A GRADIENT IN THE DEVELOPING LIMB BUD EPITHELIUM DURING TI PIONEER AXON OUTGROWTH.

SIMILARITY: Belongs to the semaphorin family.

SIMILARITY: Contains 1 Sema domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Embryo;
MEDLINE=99203450; PubMed=10101134;
Isblster C.M., Tsai A., Wong S.T., Kolodkin A.L., O'Connor T.P.;
"Discrete roles for secreted and transmembrane semaphorins in neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNUCKLE-LIKE CYSTEINE CLUSTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1; Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7DC80C97AFA93A9B CRC64;
                                                                                                                                                                                                                                                                                       | Pinch | Pinc
-!- SIMILARITY: Contains 1 engC GTPase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAX-2000 (Rel. 39, Created)
30-MAX-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Semaphorin 2A precursor (Sema 2A) (Sema II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 8.2;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               697 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTP (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schistocerca gregaria (Desert locust).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    growth cone guidance in vivo.";
Development 126:2007-2019(1999)
                                                                                                                                                                                                                                                                                 EMBL; AP001515; BAB06222.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33449 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.2%;
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133 EQLGYKVYLTSTI 145
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166
166
216
247
294 AA;
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NP_BIND
NP_BIND
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CSTRAIN=C57BL/60; TISSUE=Liver;
CMEDINE=3228822; PubMed=7683976;
Resiler K.J., Sullivan S.L., Buck L.B.;
Resiler K.J., Sullivan S.L., Buck L.B.;
Cland organization of odorant receptor gene expression in the offactory epithelium.";
Cell 73:59-609(1993).
C
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EMBL; AF134904; AAD30114.1; -.
InterPro; IPR001359; Ig.
InterPro; IPR001359; Ig.
InterPro; IPR001539; Sema; I.
SMART; SM00409; Ig. 1.
SMART; SM006409; Ig. 1.
PROSITE; PS50835; IG LIKE; 1.
SIGNAL; Immunoglobulin domain; Neurogenesis; Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7FE55AB4A965E1E4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
101-FEB-1994 (Rel. 28, Last sequence update)
101-FEB-1998 (Rel. 36, Last annotation update)
Olfactory receptor 7A (K18) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG-LIKE C2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.8%; Pred. No. 19;
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? 170 CBP4 PROTEIN.
65 65 S -> F (IN REF. 1).
170 AA; 20219 MW; D88F92EADF0B366E CRC64;
                              MITOCHONDRION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERC_NEIMA
ID SERC NEIMA STANDARD; PRT; 366
AC 034370; 033382; 033383; 033384; 033386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; ABCOSOLOS, 10. 11. 14MAP; MF 00019; -; 1. 1nterPro; IPR003664; FA_Synthesis. Pfam; PF02504; FA_Synthesis; 1. ProDom; PD006974; FA_Synthesis; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98196666; PubMed=9537320;
               Mitochondrion; Transit peptide.
TRANSIT 1 ? MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000723; AAC07145.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.08;
                                                                                                                Local Similarity 61.5%;
hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0%,
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 392:353-358(1998).
                                                                                                                                                             1 SVIAKOMTYKVYM 13
                                                                                                                                                                                        10 AVIAKOROYKHYL 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 AKQMTYKVYMSG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 AKELGYKIYLVG 37
                                                                                                                                                                                                                                                               STANDARD;
      SGD; S0003406; CBP4.
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   PLSX OR AQ_1101.
Aquifex aeolicus.
                                                                                                                                                                                                                                                  PLSX_AQUAE
ID PLSX_AQUAE
AC O67186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aeolicus
                                                             CONFLICT
                                                                            SEQUENCE
                                                                                                       Query Match
                                                CHAIN
                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                          .
0
MGD; A40745; A40745.
MGD; MGI:104712; Olfr7.
InterPro; IPR000276; GPCR_Rhodpsn.
PROSITE; PS00021; 7tm 1; 1; PROTEIN RECEP_F1 1; PARTIAL.
PROSITE; PS0022; G_PROTEIN RECEP_F1 2; 1.
G_PROTEIN COUpled receptor; Transmembrane; Multigene family; NON_TER
                                                                                                                                                                                                                                                                                            Score 39; DB 1; Length 161;
Pred. No. 7;
                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                   4 (POTENTIAL).
EXTRAGELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                 7A5140BB1EFB7FB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1994 (Rel. 30, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
18-9F4 protein, mitochondrial precursor.
CBP4 OR YGR174C.
                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=94342301; PubMed=8063753;
                                                                                                                                                                                                                                                                    17562 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U10700; AAA61566.1; -. EMBL; Z72959; CAA97200.1; -.
                                                                                                                                                                                                                                                                                               47.0%;
                                                                                                                                                                                                                                                                                                            Similarity 66.788; Conservative
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37
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98
115
139
151
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GermOnline; 141486; -.
                                                                                                                                                                                                          116
140
152 >
161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crivellone M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEMBRANE
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P37267;
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DOMAIN
TRANSMEM
                                                                                                                                                                                                DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                      NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CBP4_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Not known, probably involved in fatty acid or phospholipid synthesis (By similarity). SIMILARITY: Belongs to the plsX family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 1; Length 337;
Pred. No. 14;
Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBL_TaxID=63363;
47.0%; Score 39; DB 1;
61.5%; Pred. No. 7.3;
tive 2; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
8-EB-2003 (Rel. 41, Last annotation update)
Fatty acid/phospholipid synthesis protein plsX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 AA
                                                                                                                                                                                                                                                                                                                                                     337 AA.
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                                                                                                                                                                                                                                                                                                                                                                          STRAIN=22491 / Serogroup A / Serotype 4A;
MEDLINE=2022556; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mingall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- PATHANY: Required both in major phosphorylated pathway of serine blosynthesis and in the blosynthesis of pyridoxine.
--- SUBCELIULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                               Morelli G., Malorny B., Mueller K., Seiler A., Wang J.-F., del Valle J., Achtman M.; "Clonal descent and microevolution of Neisseria meningitidis during 30 years of epidemic spread.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A -> S (IN STRAIN Z3524).
I -> L (IN STRAINS B293, Z3524, Z3910,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aminotransférase, Pyridoxal phosphate, Complete proteome.
BINDING 203 203 PYRIDOXAL PHOSPHATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R -> C (IN STRAINS B293, Z3910 AND Z3918).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: 0-phospho-L-serine + 2-oxoglutarate
                                                                                              Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF 00160; 1.

InterPro; IPR00192; Aminotrans V.

InterPro; IPR003249; Pser amintransf.

Fram, PF00266; aminotran_5; 1.

ProDom; PD001544; Pser amintransf; 1.

TIGRFAMS; TIGR01364; SerC_1; 1.

PROSITE; PS00595; AA TRANSFER CLASS 5; 1.

Serine biosynthesis; Pyridoxine biosynthesis; Transferase;
15-DEC-1998 (Rel. 37, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
SPERC ON NMALE aminotransferase (EC 2.6.1.52) (PSAT).
SERC OR NMALE 94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphonooxypyruvate + L-glutamate.
COFACTOR: Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                         . Microbio1. 25:1047-1064(1997)
                                                                                                                                                                                                           STRAIN=Various strains;
MEDLINE=98010345; PubMed=9350862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF004820; AAC32675.1; --
EMBL; AF004821; AAC32679.1; --
EMBL; AF004822; AAC32683.1; --
EMBL; AF004823; AAC32683.1; --
EMBL; AF004824; AAC32693.1; --
EMBL; AF004825; AAC32693.1; --
EMBL; AF004825; AAC32693.1; --
EMBL; AL162757; CAB85115.1; --
PIR; F81816; F81816.
                                                                                                                                   Neisseriaceae; Neisseria.
NCBL_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 404:502-506(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aminotransferases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   meningitidis Z2491."
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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VARIANT
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Z3915 AND Z3918).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=MCS8 / Serogroup B;
MEDLINE=2010755; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark B.B.,
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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Neisseriaceae, Neisseria.
                                                                                                                                                                          47.0%; Score 39; DB 1; Length 368; 70.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD001544; Pser_amintransf; 1.
TGRRAMs; TIGR01364; serc_1; 1.
PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
Serine biosynthesis; Pytridoxine biosynthesis; Transferase; Aminotransferase; Pytridoxal phosphate; Complete protecome.
                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphoserine aminotransferase (EC 2.6.1.52) (PSAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 40, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 AA
                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP, MF 00160, -; 1.
InterPro; IPR000192; Aminotrans V.
InterPro; IPR003248; Pser amintransf.
Pfam; PF00266; aminotran 5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis (serogroup B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE002514; AAF41989.1; -. PIR; H81059; H81059; H23721; LBJN. TIGR; NMB1640; -.
                                                                                                                                                                                                  70.08;
                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                         || :|||| |
248 TYAIYMSGLV 257
                                                                                                                                                                                                                                                                                        8 TYKVYMSGTV 17
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                                                                                                                 368 AA;
                                                                                                                                                                                               Best Local Similarity
Matches 7: Conserv
  240
289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEIMB
                                                                                                                 SEQUENCE
                                                                                                                                                                          Query Match
VARIANT
VARIANT
                                                                                   VARIANT
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P57007
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  ET ET SO
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Gaps

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BINDING SEQUENCE Query Match

Matches

ð g RESULT 11 SP98 YEAST

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-!- PATHWAY: Biosynthesis of penicillin and cephalosporin, first step.-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enkaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; mitosporic Hypocreaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gutierrez S., Diez B., Montenegro B., Martin J.F., Gutierrez S., Diez B., Montenegro B., Martin J.F., Gutierrez S., Diez B., Montenegro B., Martin J.F., Gutierration of the Cephalosporium acremonium pcbAB gene encoding alpha-aminoadipyl-cysteinyl-valine synthetase, a large multidomain peptide synthetase: linkage to the pcbC gene as a cluster of early cephalosporin biosynthetic genes and evidence of multiple functional domains.";
GO; GO:0005822; C:inner plaque of spindle pole body; IDA.
GO; GO:0005824; C:outer plaque of spindle pole body; IDA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IPI.
GO; GO:0007020; P:mitotic spindle assembly (sensu Saccharomyces); IMP.
GO; GO:000071; P:mitotic spindle assembly (sensu Saccharomyces); InterPro; IRR007259; Spc97. Spc98.
InterPro; IRR007259; Spc97. Spc98.
Microtubule; Nuclear protein.
SEQUENCE 846 AA; 98226 MW; 803048B05D5E5105 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intermediates
-!- CATALYTIC ACTIVITY: L-2-aminohexanedioate + L-cysteine + L-valine
+ 3 ATP = N-[L-5-amino-5-carboxypentanoyl]-L-cysteinyl-D-valine +
3 AMP + 3 diphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoskins J.A., O'Callaghan N., Queener S.W., Cantwell C.A., Wood J.S., Chen V.J., Skatrud P.L., "Gene disruption of the pcbAB gene encoding ACV synthetase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cephalosporium acremonium.";

Curr. Genet. 18:523-530(1990).
-!- FUNCTION: Each of the constituent amino acids of the tripeptide pry are activated as aminoacyl-adenylates with peptide bonds formed through the participation of amino acid thiolester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
14 (-Samino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase
(RC 6.3.2.26) (Delta (L-alpha aminoadipyl)-L-cysteinyl-D-valine
synthetase) (ACV synthetase) (ACVS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: Contains 3 covalently bound phosphopantetheines
                                                                                                                                                                                                                                                Score 39; DB 1; Length 846;
pred. No. 35;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cephalosporium acremonium (Acremonium chrysogenum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=ATCC 11550;
MEDLINE=91168300; PubMed=2076552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: Contains 3 acyl carrier domains. PIR, A38531, YGCBYC.
HSSP, P14687, IAMU.
InterPro; IPR000873; AMP-bind.
InterPro; IPR001242; Condensatn.
InterPro; IPR001242; Condensatn.
InterPro; IPR00163; Pp bind.
InterPro; IPR00163; Ppintne_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 3712 AA
                                                                                                                                                                                                                                                          47.0%; Score 39;
46.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 173:2354-2365(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=91177827; PubMed=1706706;
                                                                                                                                                                                                                                                                                 46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                       394 IPKELAYKIFMIG 406
                                                                                                                                                                                                                                                                                                                                                         3 IAKQMTYKVYMSG 15
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Potential)
                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEPAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P25464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
ACVS_CEPAC
                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHĀRACTERIZATION.
MEDLINE=96324398; PubMed=8670895;
Geissler S., Pereira G., Spang A., Knop M., Soues S., Kilmartin J.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        microtubule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microtubule attachment.";
EMBO J. 15:3899-3911(1996).
-!- FUNCTION: Involved in microtubule organization by the microtubule organizing centre, the spindle pole body (SPB). Probably part of the microtubule attachment site at the SPB.
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D.,
Pallavicini A., Lanfranchi G., Valle G.;
"The DNA sequence of cosmid 14-13b from chromosome XIV of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The spindle pole body component Spc98p interacts with the gamma-tubulin-like Tub4p of Saccharomyces cerevisiae at the sites migratuhyle attachmort ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96109932; PubMed=8619318;
Mallet L., Bussereau F., Jacquet M.;
"A 43.5 Kb segment of yeast chromosome XIV, which contains MFA2,
MEP2, CAP/SRV2, NAM9, FKB1/FPR1/RBP1, WOM22 and CPT1, predicts an
adenosine deaminase gene and 14 new open reading frames.";
Yeast 11:1195-1209(1995).
                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 4) Last annotation update)
Spindle pole body component SPC98.
Spindle pole body romponent SPC98.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycetes;
               PYRIDOXAL PHOSPHATE (BY SIMILARITY) 97DFCE52BBE5E021 CRC64;
                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae reveals an unusually high number of overlapping open reading frames."; Yeast 13:261-266(1997).
                                                                                       Score 39; DB 1; Length 368;
Pred. No. 16;
                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: Interacts with TUB4 and SPC97.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the GCP family.
                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=97245296; PubMed=9090055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z46843; CAA86899.1; -.
EMBL; Z69382; CAA93378.1; -.
EMBL; Z71402; CAA96007.1; -.
PIR; S59262; S59262.
GermChline; 143132; -.
SGD; S0005070; SPC98.
                                           41393 MW;
                                                                                                                70.08;
                                                                                            47.08;
                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                        248 TYAIYMSGLV 257
                                                                                                                                                                                             8 TYKVYMSGTV 17
                       203
368 AA;
                                                                                                                   Local Similarity
nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=S288c;
                                                                                                                                                                                                                                                                                                                                                            SP98 YEAST
P53540;
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us-09-890-463-2.rsp

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STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli, a
Escherichia coli 06
                                                                                                                                                                                                                                             Local Similarity
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                                                        PIR; A69445; A69
TIGR; AF1562; -.
                                                                                                                                                                 TRANSMEM
SEQUENCE
                                                                                                                                                                                                                            Query Match
                                                                                                                                           TRANSMEM
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                 SO FIT EXE
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SEQUENCE FROM N.A.
SEQUENCIS FOR 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Klenk H.-P., Clayton R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Ariach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHOPANTETHEINE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                      DOMAIN 1 (ADIPATE-ACTIVATING).
DOMAIN 2 (CYSTEINE-ACTIVATING).
DOMAIN 3 (VALINE-ACTIVATING).
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 1; Length 3712;
Pred. No. 1.5e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    THIOESTERASE (BY SIMILARITY).
                                                                                                                                                                                                           Ligase; Antibiotic biosynthesis; Multifunctional enzyme; Repeat; Phosphopantetheine.
REPEAT 234 1062 DOMAIN I (ADIPATE-ACTIVATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3712 AA; 414767 MW; 4EE3C1EB5EBEF9B7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHOPANTETHEINE
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                            PRINTS; PRO0154; AMPBINDING.
PROSITE; PSO0012; PHOSPHOPANTETHEINE; 2.
PROSITE; PSO0455; AMP BINDING; 3.
PROSITE; PS50075; ACP_DOMAIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
InterPro; IPR000379; Ser_estrs.
InterPro; IPR001031; Thioesterase.
Ffam; PP00601; AMP-binding; 3.
Pfam; PP00668; Condensation; 3.
Pfam; PP00550; pp-binding; 3.
Pfam; PP00975; Thioesterase; 1.
                              Thioesterase.
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Matches 7; Conservative
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1916
2990
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3568
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SEQUENCE
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DOMAIN
BINDING
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DOMAIN
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Lindquist S., Weston-Hafer K., Schmidt H., Pul C., Korfmann G.,
Erickson J., Sanders C., Martin H.H., Normark S.;
"AmpG, a signal transducer in chromosomal beta-lactawase induction.";
Mol. Microbiol. 9:703-715(1993).
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MEDLINE-22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.
Riley M., Collado-Vides J., Glaener J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                           ٠,
                                                                                                                                                                                                                                                                                                                            45.8%; Score 38; DB 1; Length 140; 37.5%; Pred. No. 9.3; ive 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12.";
                                                                                                            Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 20 42 POTRNTAL
                                                                                                                                                                                                                                                         140 AA; 15667 MW; 937DCB5585A17991 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YAJG ECOLI STANDARD, PRT, 192 AA. B3671, P77210; Created) O1-UNV-1994 (Rel. 29, Created) 10-UNV-1994 (Rel. 29, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Hypothetical lipoprotein yajG precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Probable).
-!- SIMILARITY: TO H.INFLUENZAE HI0162.
                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                           POTENTIAL
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NCBI_TaxID=562, 217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VIAKQMTYKVYMSGTV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 IIFMAITFAIYVSGTL 44
EMBL; AE000994; AAB89687.1;
PIR; A69445; A69445.
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                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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Youvan D.C., Bylina E.J., Alberti M., Begusch H., Hearst J.E.;
"Nucleotide and deduced polypeptide sequences of the photosynthetic reaction-center, B870 antenna, and flanking polypeptides from R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
CHARACTERIZATION.
TARAIN-SBB1003 / CB1029;
MEDLINE-2031966; PubMed=10811655;
Fujita Y., Bauer C.E.,
"Reconstitution of light-independent protochlorophyllide reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-palmitoyl cysteine (Potential).
S-diacylglycerol cysteine (Potential)
9E9E6568E9253451 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
88-FBB-2003 (Rel. 41, Last amnotation update)
Light-independent protochlorophyllide reductase iron-sulfur ATP-binding protein (EC 1.18.-.-) (LI-POR subunit L) (DPOR subunit L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL LIPOPROTEIN YAJG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Membrane; Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacteriochlorophyll biosynthetic pathway.";
J. Bacteriol, 172:5001-5010(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                          EMBL; S67816; AAB28883.2; -... EMBL; AE001019; AAG73537.1; ALT INIT. EMBL; AE0010199; AAG73537.1; ALT INIT. EMBL; AE016756; AAN79024.1; ALT INIT. EMBL; AE016756; AAN79024.1; ALT INIT. BCodene; BG12182, YajG.
InterPro; IPR005619; Lipoprotein 16; InterPro; IPR000437; Prok lipoprotein 26; Probom; PD036382; Lipoprotein 16; 1... PRODOM; PD036382; Lipoprotein 16; 1... PROSITE; PS00013; PROKAR LIPOPROTEIN; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38;
Pred. No.
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MEDLINE=90368552; PubMed=2203738;
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83 VLEKOMTARGYMVG 96
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18
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ses 8; Conserv
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P26237;
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BCHL_RHOCA
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                                                                                                                                                                                                                                    Unpublished observations (JUL-2001).

--- FUNCTION: Uses Mg-ATP and reduced ferredoxin to reduce ring D of protechlorophyllide (Pchilde) to form chlorophyllide a (Chlide).

This reaction is light-independent.
--- PATHWAY: Light-independent bacteriochlorophyll biosynthesis.
--- SHENUIT: Protechlorophyllide reductase is thought to be composed of three subunits; both, both and bohs. Homedimer of both subunit.

(By similarity).
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from purified bohl and bohN-bohB subunits. In vitro confirmation of nitrogenase-like features of a bacteriochlorophyll biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the nifH / bchL / chlL family.
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EMBL; Z11165; CAA77523.1; -.
EMBL; X01183; -; NOT_ANNOTATED_CDS.
PIR; B36716; B36716.
PIR; H28771; H28771.
HSSP; P00456; 1CP2.
HAMAP; MR 00355; -; 1.
InterPro; TPR000392; NitrogenaseII.
InterPro; TPR005971; Protochl_reductF.
PERM; PF00142; fer4_NifH; 1.
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Pred. No.
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                                                                                                         J. Biol. Chem. 275:23583-23588(2000)
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TIGREAMS; TIGROISSI, DOPR BCHL, 1.
PROSITE; PSO0746; NIFH FRXC 1; 1.
PROSITE; PSO0692; NIFH—FRXC 2; 1.
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198 AVQAKSVNYKVRLAGCV 214
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                                                                                                                          August 12, 2004, 06:12:47; Search time 4.42418 Seconds
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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3: Sp fungi:*
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098921 bacillus ha 0888m2 pseudomonas 09suc1 arabidopsis 09yrs6 anabaena sp 091vn1 arabidopsis 09rs9 neisesia m	neisseria neisseria neisseria neisseria neisseria neisseria neisseria	052465 neisseria m 052467 neisseria m 052468 neisseria m 052468 neisseria m 054532 neisseria m 055485 radianthus 080740 borrelia bu 09474 lactococcus 09474 lactococcus 09474 lactococcus 084778 chlamydia t 084778 chlamydia t 084778 chlamydia t 084178 neisseria g	ALIGNMENTS	PRT; 221 AA.  Created)  Last sequence update)  Last annotation update)  ia; Anthozoa; Zoantharia; Scleractinia;  1682051;  Terskikh A., Matz M.V., Labas Y.A.,  T.G., Lukyanov K.A., Lukyanov S.A.;  s a source of far-red fluorescent   fluoresin:  fluoresin:  protein:  prote
Q9K9Z1 Q888M2 Q9SUC1 Q8YTR6 Q9LVN1 Q9R2Y3	052461 052461 052462 052463 052463 052463 052464	052465 052466 052466 052468 0524885 054532 089788 050740 090778 09PLF0	ALIGN	THRY; PRT; 221 Fel. 19, Created) Fel. 19, Last sequence Fel. 25, Last annotation Cnidaria; Anthozoa; Zo Goniopora.  DMed=11682051;  DW A.F., Terskikh A., hevich Y.G., Lukyanov Felns as a source of fa (2001). 7542.1; Fergy pathways; IEA. GFP like. Green_fl_protein. 1. 24918 MW; 93F9F4B5C20
	000000000	2211 9 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		19, 19, 19, 10, 11, 11, 11, 11, 11, 11, 11, 11, 11
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			<u>κ</u> ο	SPRARRARRARRASS

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Gaps

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100.0%; Score 83; DB 5; Length 221; 100.0%; Pred. No. 1.3e-06; Live 0; Mismatches 0; Indels

1 SVIAKOMTYKVYMSGTV 17 SVIAKQMTYKVYMSGTV 18

ð

RESULT 2 Q97LU2

Q7XDZ1 Q9KBK0

**Q97FT4** 

17; Conservative

Matches

Query Match Best Local Similarity

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Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL13360; CAB63761.1; -. PIR; 743498; 743498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harris P.C.; "PARTILI, a homolog of the autosomal recessive polycystic kidney disease gene, encodes a receptor with inducible I lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22508206; PubMed=12620974;
Hogan M.C., Griffin M.D., Rossetti S., Torres V.E., Ward C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.8%; Score 43; DB 4; Length 4243; 43.8%; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4243 AA; 465745 MW; 36FE9DE63F4931E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 AA; 46402 MW; 35523FD7C62313A2 CRC64;
                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Fragment).
DKFZPS86C1021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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424 AA.
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Hum. Mol. Genet. 12:685-698(2003).
EMBL; AV219181; AAO66072.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR00299; IPT TIG.
InterPro; IPR00626; PbHI.
Pfam; PP01833; TIG; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
PRT;
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1 SIVALNKSYEVYFTGT 16
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Best Local Similarity 43.0.
Local 7; Conservative
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SMART; SM00710; PbH1; 10
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PRELIMINARY;
                                                                                                                                                                                          Homo sapiens (Human)
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les 7; Conserv
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SEQUENCE FROM N.A.
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SEQUENCE
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Q9UF27
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ID Q8
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                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

MEDLIND=21359325; PubMed=11466286;

MEDLIND=21359325; Dubed=11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stramm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing

bacterium Clostridium acetobutylicum.";

J. Bacterium 183:4823-4838(2001).

EMBL, AR007561; AAK78442.1;

PIR; G96956; G96956.
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MEDLINE=21664373; PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                       Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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Pred. No. 32;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.2%; Score 45; DB 16; Length 398; 47.1%; Pred. No. 14; 7; Indels ive 2; Mismatches 7; Indels
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EMBL; AP003192; BABB1780.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 389 AA; 43138 WW; 36E1230CC803E7C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398 AA; 45650 MW; 59324A21CA466DFC CRC64;
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CPE2074.
                                                                                       01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Protein of short-chain alcohol dehydrogenase family
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           398 AA
                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 SYIGSPRTYKIYREGTI 240
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Best Local Similarity 47.1%;
Matches 8; Conservative
                                  097LU2;
01-OCT-2001 (TrEMBLrel. 18,
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Best Local Similarity 41.*.
T; Conservative
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           PRELIMINARY;
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RESULT 3

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4; Indels

Length 424;

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Gaps

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4; Indels

227 AA.

PRT:

PRELIMINARY;

Q8MU45

RESULT 4 Q9UF27

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TIGRPAMS; TIGRO1135; glms; 1.
PROSITE; PS00443; GATASE TYPE II; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 592 AA; 65796 MW; 3CED613D9A0EB7ED CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             592 AA.
                                                                                                                                                                                                     FEBS Lett. 507:16-20(2001).

EMBL, AF363775; AAL27537.1; -.

GO; GO:0006091; P:energy pathways; IEA.

InterPro; IPR009017; GFP like.

InterPro; IPR000786; Green_fl_protein.
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                                                                                                                  SEQUENCE FROM N.A. MEDLINE=21538626; PubMed=11682051;
                                                                                                                                                                                                                                                                                                                                                                                                                      2 VIAKQMTYKVYMSGTV 17
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Pfam; PF01380; SIS; 2.
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Matches 7; Conserv
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                                                                                      NCBI_TaxID=47073;
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Q96YI5
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                                                Green fluorescent protein-like protein.
Condylactis gigantea (Giant anemone).
Eukaryota; Metazoa; Chidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Condylactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Condylactis.
NCBI_TaxID=175772;
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                                                                                                                                                     Matz M.V., Lukyanov S.A.;
"Diversity and evolution of GFP-like fluorescent proteins.";
"Diversity and evolution of GFP-like fluorescent proteins.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBU databases.

GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
PinerPro; IPR009017; GFP like.
Pfam; PF01353; GFP; 1.
ProDom; PD013756; Green_fl_protein; 1.
                                                                                                                                                                                                                                                                                                                           5; Length 227;
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                                                                                                                                                                                                                                                                           227 AA; 25384 MW; D3C6B02F490F3D21 CRC64;
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 227 AA; 25446 MW; E51CC017108593E3 CRC64;
    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
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FRES Lett. 507:16-20(2001).
EMBL, AF383155; AAL27541.1;
GO: GO: 00006091; P: energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR00786; Green fl protein.
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01-DEC-2001 (TrEMBLrel. 19, Created)
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4 LLKESMRIKIYMEGTV 19
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Best Local Similarity 43.57
Conservative
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Best Local Similarity 43.0%
Local 5; Conservative
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                                                                                                              NCBI_TaxID=47073;
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MEDLINE-21456156; PubMed=11572479;

Rawarabagyasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Rawarabagyasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Ragai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

Radi Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

Roshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oquchi A.,

Radi K.-I., Msuda S., Yanagii M., Nishimura M., Yamagishi A.,

Shima T., Kikuchi H.;

Complete genome sequence of an aerobic thermoacidophilic

Complete genome sequence of an aerobic thermoacidophilic

Complete genome sequence of an aerobic thermoacidophilic

DNA Res. 8:123-140(2001)

BNA Res. 8:123-140(2001)

BNA Res. 8:123-140(2001)

CO:0000999; BAB67292.1; -.

CO:00004560; F:glutamine-fructose-6-phosphate transaminase. ..; IEA.

CO: GO:0004560; F:glutamine-fructose-6-phosphate transaminase. ..; IEA.

CO: GO:0004560; F:glutamine-fructose-6-phosphate transaminase. ..; IEA.

CO: GO:0004560; F:glutamine-fructose-6-phosphate transaminase. ..; IEA.

RO: GO:0005529; F:sugar binding; IEA.

RO: GO:0005529; F:sugar binding; IEA.

RO: GO:0005529; F:sugar binding; IEA.

RITHEFPO: IPRO05855; GlmS.

RITHEFPO: IPRO05855; GlmS.

RITHEFPO: IPRO05855; GlmS.

RITHEFPO: IPRO05855; GlmS.
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GFP-like chromoprotein.
Condylactis gigantea (Giant anemone).
Eukaryota; Metazoa; Chidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Condylactis.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative glucosamine--fructose-6-phosphate aminotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 227;
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ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 227 AA; 25416 MW; BCFASA4CBCE1B3F7 CRC64;
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SPECIES=L.lactis (subsp. lactis); STRAIN=IL1403; MEDLINE=21235186; PubMed=11337471; Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403."; Genome Res. 11:731-753(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fluorescent protein FPS83.
Discosoma sp.
Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus lactis (subsp. lactis) (Streptococcus lactis), and Lactococcus lactis.

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-L.lactis; STRAIN=IL1403;
TRANSPOSON=transposon-like element TnX;
Calero S., Ehrlich S.D., Jamet B., Bolotin A., Renault P.;
Calero S., Ehrlich S.D., Jamet B., Bolotin A., Renault P.;
Characterization of the two genes encoding histone-like proteins of the HU family in Lactococcus lactis IL1403.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AE06205; AAK04599.1;
EMBL; AE06205; AAK04599.1;
FIR; B86687; B86687.
SPEC, B86687; B86687;
SPEC, B86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bolotin A., Mauger S., Malarme K., Ehrlich S.D., Sorokin A., "Low-redundancy sequencing of the entire Lactococcus lactis IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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Pred, No. 60;
Length 3583;
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                                                                         Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypottical protein yfaA.
YFAA OR LL0501.
49.4%; Score 41; DB 2;
43.8%; Pred. No. 7e+02;
Live 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIESE.L. Lactis, STRAIN=IL1403;
SPRECIESE.L. Tactis, STRAIN=IL1403;
MEDLINE=20000172; PubMed=10532372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antonie Van Leeuwenhoek 76:27-76(1999)
                                                                                                                                                                                                48.2%;
70.0%;
                                                                                                                                                  1 SVIAKOMTYKVYMSGT 16
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Matches 7; Conservative
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                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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   Query Match
Best Local Similarity
Matches 7; Conserv
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1D 09
AC 09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fuma S., Fujishima Y., Corbell N., D'Souza C., Nakano M.M., Zuber P., Yamane K.;
"Nucleotide sequence of 5' portion of srfA that contains the region required for competence establishment in Bacillus subtilis.";
Nucleic Acids Res. 21:93-97(1993).
BMBL; X72672; CAA51223.1;
HSSP; P14687; 1AMU.
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U -> R (IN REF. 2).
V -> C (IN REF. 2).
T -> S (IN REF. 2).
G -> R (IN REF. 2).
R -> C (IN REF. 2).
R -> A (IN REF. 2).
L -> A (IN REF. 2).
A -> P (IN REF. 2).
A -> D (IN REF. 2).
B -> D (IN REF. 2).
C -> P (IN REF. 2).
C -> P
                                              Score 41; DB 17; Length 592;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fabret C., Quentin Y., Guiseppi A., Busuttil J., Haiech J.,
                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Surfactin synthetase.
Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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GO; GO:0008152; P:metabolism; IEA.
InterPro; IPRO00873; AMP-bind.
InterPro; IPRO0162; Ppantne_S.
InterPro; IPRO06162; Ppantne_S.
InterPro; IPRO06162; Ppantne_S.
Fam; PF005610; AMP-binding; 3.
Pfam; PF00560; Condensation; 4.
Pfam; PF00560; pp-binding; 3.
Pfam; PF00550; pp-binding; 3.
Pfam; PR00154; AMPBINDING.
PROSITE; PS50075; ACP_DOMAIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 3583 AA
                                                                                                                           3; Mismatches
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PROSITE; PS00455; AMP_BINDING; 3.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 3.
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MEDLINE=93181186; PubMed=8441623;
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MEDLINE=95219089; PubMed=7704264;
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                                                      49.4%;
53.8%;
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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SAIARESDYKIYM 391
                   Query Match
Best Local Similarity 53.8.
Tr Conservative
                                                                                                                                                                                                        SVIAKOMTYKVYM 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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2542
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SEQUENCE
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245675
AC Q45675
DT Q4567
DT Q1-NO
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DT 01-NO
DT 01-NO
DT 01-NO
DE Bacte
OX NOEI
RR Bacill
RA Fabre
RR SEQUE
RR HAMBDLI
RA Fabre
RR HAMBLI
RR CONFERENCE
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Hypothetical protein CAC2643.
CAC2643.
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                                                                                                                                                                                                                    Clostridium acetobutylicum
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                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                   01-OCT-2001
01-JUN-2003
                                                                                                               01-OCT-2001
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                                                                                              Q97FT4
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                              RESULT 14
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Q7XDZ1
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Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia;
Discosomatidae; Discosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                               MEDLINE-99436614; Pubmed-10504696;
Matz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G.,
Markelov M.L., Lukyanov S.A.;
                                                                                                                                                                                                                         Markelov M.L., Eradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G., Markelov M.L., Lukyanov S.A.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF168419, AF703369.1; -.. PDB; 1G7K; 07-NOV-01.
                                                                                                                                         "Fluorescent proteins from nonbioluminescent Anthozoa species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Novel fluorescent protein from Discosoma coral and its mutants possesses a unique far-red fluorescence."; FEBS Lett. 479:127-130(2000). EMBI; AF27271; AAG16224-1; -HSSP; P42212; 1BFP.
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Fradkov A.F., Chen Y., Ding L., Barsova E.V., Matz M.V.,
Lukyanov S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 225 AA; 25931 MW; FBF9A5369778F689 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 230 AA; 26370 MW; 5215B1B436D67E51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                   Nat. Biotechnol. 17:969-973(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SVIAKOMTYKVYMSGTV 17
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6 NVIKEFMRFKVRMEGTV 22
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  Discosomatidae, Discosoma
NCBL_TaxID=86600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 52.3.
Best Local 9; Conservative
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                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=137428;
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                                                                                                                                                                                                                                                                                                                                                      STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE=21359325; PubMed=11466286;

MeDLINE=21359325; PubMed=11466286;

Gibsolling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin B.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";

J. Bacterium (193:4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                     Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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The Rice Chromosome 10 Sequencing Consortium;
"In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.2%; Score 40; DB 16; Length 263; 43.8%; Pred. No. 72; 1ve 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

48.2%; Score 40; DB 10; Length 268;
Best Local Similarity 57.1%; Pred. No. 74;
Matches 8; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41D648F7237A42AB CRC64;
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                                                 (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative AP2-domain DNA-binding protein.
263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE007761; AAK80590.1; -...
PIR; C97225; C97225.
PYPOthetical protein; Complete proteome.
SEQUENCE 263 AA; 29220 MW; 410648F77.
  PRT;
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λ O

3 IAKQMTYKVYMSGT 16 : | | | | | | | | | 94 LLKIMIYKVYADGT 107

Search completed: August 12, 2004, 06:19:35 Job time: 7.67418 secs

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(without alignments)
149.169 Million cell updates/sec
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                                                                                                                                                                                            August 12, 2004, 06:19:43 ; Search time 35.7766 Seconds
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2: (egn2_6/ptodata/2/pubpaa/USO6_MW_PUB.pep:*
4: (egn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: (egn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: (egn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: (egn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
7: (egn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
8: (egn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: (egn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
10: (egn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: (egn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
12: (egn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
14: (egn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
15: (egn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: (egn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: (egn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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17: (egn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: (egn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: (egn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: (egn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1292805 seqs, 313927144 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                             - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                               1 SVIAKOMTYKVYMSGTV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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83
                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                             OM protein
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                        Run on:
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		Description	Sequence 43, Appl	Segmence 172498	9	Sequence 7, Appli	Segmence 8. Appli	Segmence 25. April	Segmence 46. April	Segment 67 April	Segmence 12 April	Sequence 12. Anni	Segmence 12. April	Semience 4 Appli	Semience 12 Annual	Segience 44 April	Sequence 8, Appli
		ID	US-09-994-595-43	US-10-424-599-172498	US-10-315-920-6	US-10-442-148A-7	US-10-442-148A-8	US-10-081-864-25	US-10-006-922-46	US-09-999-745-67	US-09-866-538-12	US-09-794-308-12	US-09-865-291-12	US-10-132-067-4	US-10-006-922-12	US-10-006-922-44	US-10-081-864-8
		1	10	12	14	15		14			10	10	10	12	13	13	14
		Match Length DB	107	47	225	225	239	26	205	225	225	225	225	225	225	225	225
ℴ	Query	Match	51.8	9.05	49.4	49.4	49.4	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2
		Score	43	42	41	41	41	40	40	40	40	40	40	40	40	40	40
	Result	No.	г	0	e	4		9	7	80	6	10	11	12	13	14	15

Segmence 12. Appl	1.	20.	2	Sequence 4, Appli	26	32	13,								Sequence 112625,		7	Sequence 52, Appl	m	76	80,	224	_		17	41,	ω,	10	Sequence 26, Appl
4 US-10-081-864-12	4 US-10-121-258-1	4 US-10-121-258-20	4 US-10-315-920-2	4 US-10-315-920-4	5 US-10-370-570-56	5 US-10-406-618-32	6 US-10-433-640-13	6 US-10-724-178-12	3 US-10-006-922-18	4 US-10-161-403-40	6 US-10-314-936-2	5 US-10-314-936-4	US-10-152-	US-10-739	6 US-10-437-963-112625	5 US-10-343-977-1	5 US-10-343-977-2	4 US-10-214-932-52	5 US-10-343-977-3	4 US-10-214-932-76	0 US-09-994-595-80	2 US-10-424-599-224455		4 US-10-155-809-8		5 US-10-423-688A-41	US-09-976-673-8	US-09-976-673-10	US-09-976-673-26
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48.2	48.2	•	48.2	48.2	48.2	48.2	48.2		48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	47.0	•	47.0	٠.	47.0	47.0	47.0	47.0	47.0
40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	39	33	33	39	39	39	39	39	39
16	17	18	13	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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RESULT 1
US-09-994-595-43
Sequence 43, Application US/09994595
Sequence 43, Application US/09994595
Publication No. US20030039981A1
APPLICANT: Bhattacharjee, J.
APPLICANT: Bhattacharjee, J.
APPLICANT: Bhattacharjee, Jaser
TITLE OF INVENTION: AD BLOGICAL SAMPLE
FILE REFERENCE: 96,247-A
CURRENT APPLICATION NUMBER: 08/09/994,595
CURRENT FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 160
SOUTHWARE: Microsoft Word 97
SEQ ID NO 43
FRINKE: Microsoft Word 97
SEQ ID NO 43
CURRENT PILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 160
SOUTHWARE: Microsoft Word 97
SEQ ID NO 43
CURTY MACH
SEQ ID NO 43
ALENGTH: 107
TYPE: PRT
CURRENTE: PRINKE: Microsoft Word 97
SEQ ID NO 43
SEQ ID NO 43
SEQ ID NO 43
SEQ ID NO 43
SEQ ID NO 44
SEC ID 44-59-172498
SEC ID NO 44
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SEC ID 44-59-172498
SEC ID 44-59-172498
SEC ID 44
SEC ID 44-59-172498
SEC ID 44-59-172498
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein sequence
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ORIENTATION-CONTROLLED PROTEIN AND TITLE OF INVENTION: PROCESS FOR IMMOBILIZING PROTEIN USING THE SAME FILE OF INVENTION: PROCESS FOR ARRAYING AND IMMOBILIZING PROTEIN USING THE SAME FILE REFERENCE: 04583.0103-0000 CURRENT APPLICATION NUMBER: US/10/442,148A CURRENT FILING DATE: 2002-05-21 PRIOR APPLICATION NUMBER: JP 2002-148950 PRIOR FILING DATE: 2002-05-23 NUMBER OF SEQ ID NOS: 12 SEQ ID NOS: 12 SEQ ID NO 7 ILENGTH: 225 SEQ ID NO 7 ILENGTH: 225
                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein sequence US-10-442-148A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: IMEGRA, MASAHIRO
APPLICANT: INTEGRA, KIYONORI
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ORIENTATION-CONTROLLED PROTEIN AND
TITLE OF INVENTION: PROCESS FOR ARRAYING AND IMMOBILIZING PROTEIN USING THE SAME
FILE REPRENCE: 04593.0103-00000
CURRENT APPLICATION NUMBER: US/10/442,148A
CURRENT PILING DATE: 2003-05-21
PRIOR FILING DATE: 2002-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-081-864-25

Sequence 25, Application US/10081864

Sequence 25, Application US/10081864

Sequence 25, Application OS US2030022287A1

Sequence 25, Application No. US2003022287A1

SEMENTALICANT: Lukyanov, Sergey

APPLICANT: Lukyanov, Konstantin

APPLICANT: Lukyanov, Konstantin

APPLICANT: Savistky, Alexandr

APPLICANT: Savistky, Alexandr

APPLICANT: Savistky, Alexandr

TITLE OF INVENTION: Methods for Using the Same

FILE REFERENCE: CLON-067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    DB 15; Length 225; 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
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49.4%; Score 41;
Best Local Similarity 52.9%; Pred. No.
Matches 9; Conservative 3; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/10442148A Publication No. US20040014242A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SVIAKOMTYKVYMSGTV 17
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SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Best Local Similarity
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LENGTH: 239
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       APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38-21(53.23.8)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 172498
LENGTH: 47
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APPLICANT: Frackov, Arcady Pedorovich
APPLICANT: Terskikh, Alexey
TITLE OF INVENTION: FLOCRESCENT TIMER PROTEINS AND METHODS
TITLE OF INVENTION: FOR THEIR USE
TITLE OF INVENTION: FOR THEIR USE
CURRENT APPLICATION UNMERS: US/10/315,920
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 60/211,607
PRIOR APPLICATION NUMBER: PCT/USO1/19097
PRIOR APPLICATION NUMBER: PCT/USO1/19097
PRIOR PILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: variant of sequence from Discosoma sp US-10-315-920-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_126782C.1.pep
US-10-424-599-172498
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Pred. No. 2.8;
4; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(47)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/10442148A Publication No. US20040014242A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-315-920-6
; Sequence 6, Application US/10315920
; Publication No. US20030175809A1
; GENERAL INFORMATION:
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16 VARQPTIRIYMLGT 29
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Best Local Similarity 50.v.
7, Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
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6 NVIKEFMRFKVRMEGTV
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ORGANISM: Discosoma sp.
US-09-999-745-67
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
          GENERAL INFORMATION:
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US-09-794-308-12
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LENGTH: 225
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APPLICANT: Lukyanov, Sergey A

APPLICANT: Lukyanov, Arcady F.

APPLICANT: Lubas, Wuli A.

APPLICANT: Labas, Yuli A.

APPLICANT: Matz, Mikhail V.

APPLICANT: Terskikh, Alexey

TITLE OF INVENTION: No. US20020197676Alel Chromophores/Fluorophores and

TITLE OF INVENTION: No. US2020197676Alel Chromophores/Fluorophores and

TITLE OF INVENTION: No. US2020197676Alel Chromophores/Fluorophores and

FILE REFERENCE: CLON-035CIP

CURRENT APPLICATION NUMBER: US/10/006,922

CURRENT FILING DATE: 2001-12-04

PRIOR FILING DATE: 1998-12-09

PRIOR APPLICATION NUMBER: 09/458,477

PRIOR APPLICATION NUMBER: 09/458,477

PRIOR APPLICATION NUMBER: 09/458,477

PRIOR PILING DATE: 1999-12-09

PRIOR PILING DATE: 1999-11-19
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
48.2%; Score 40; DB 14; Length 26;
Best Local Similarity 52.9%; Pred. No. 3.3;
Matches 9; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: non-aggregating mutant fragment
US-10-081-864-25
     CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: 10/006,922
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SSQ ID NO 25
LENGTH: 26
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SOFTWARE: FastSEQ for Windows Version 4.0
CURRENT APPLICATION NUMBER: US/10/081,864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-10-006-922-46
; Sequence 46, Application US/10006922
; Publication No. US20020197676A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 NVIKEFMRFKVRMEGTV 22
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                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Discosoma species
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; Sequence 67, Application US/0999745; Patent No. US20020157120A1

US-09-999-745-67

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APPLICANT: THE RECENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Tsien, Roger Y.
APPLICANT: Tsien, Roger Y.
APPLICANT: Baind, Geoffrey
ITILE OF INTENTION: CIRCULABLY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: REGEN1470-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/316,920
PRIOR APPLICATION NUMBER: 09/316,920
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 225;
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; Sequence 12, Application US/09866538
; Publication No. US20030032088A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                 48.2%; Score 40; DB 9; 52.9%; Pred. No. 38;
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Publication No. US20030170911A1
GENERAL INFORMATION:
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LENGTH: 225
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                                                                                                                                                                                                      GENERAL INVENTATION:
GENERAL INVENTATION:
GENERAL INVENTATION:
GENERAL INVENTATION:
APPLICANT: Pradkov, Arcady F.
APPLICANT: Labas, Yulii A.
APPLICANT: Tarakov, Arcady F.
APPLICANT: Tarakikh, Alexey
TITLE OF INVENTION: No. US20020197676A1el Chromophores and
TITLE OF INVENTION: No. US20020197676A1el Chromophores and
TITLE OF INVENTION: No. US20020197676A1el
CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR PRILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR PLING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR APPLICATION NUMBER: 09/454,338
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
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3; Mismatches
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                                                                                                                               Sequence 12, Application US/10006922
Publication No. US20020197676A1
GENERAL INFORMATION:
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6 NVIKEFMRFKVRMEGTV 22
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US-10-006-922-44
                                                                                                           US-10-006-922-12
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US-09-865-291-12
; Sequence 12, Application US/09865291
; Perulication No. US20030186229A1
; Publication No. US20030186229A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSIEN, ROGER
; APPLICANT: TING, Alice
; APPLICANT: THENG, Alice
; APPLICANT: EMANG, Jin
; TILLE OF INVENTION: EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
; FILE REPERENCE: REGENISSO
; CURRENT APPLICATION NUMBER: US/09/865,291
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                       Gaps
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Sequence 4, Application US/10132067

Publication No. US20030203355A1

GENERAL INFORMATION:
APPLICANT: Bradbury, Andrew
APPLICANT: Waldo, Geoffrey
APPLICANT: Waldo, Geoffrey
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fluorescence
TITLE OF INVENTION: Fluorescence
TITLE OF INVENTION: Fluorescence
TITLE OF INVENTION: Pluorescence
CURRENT APPLICATION NUMBER: US/10/132,067

CURRENT APPLICATION NUMBER: 202-04-24

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.1

LENGTH: 225
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48.2%; Score 40; DB 12; Length 225;
Best Local Similarity 52.9%; Pred. No. 38;
Matches 9; Conservative 3; Mismatches 5; Indels
                                                                                                        48.2%; Score 40; DB 10; Length 225; illarity 52.9%; Pred. No. 38; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.2%; Score 40; DB 10; Length 225; 52.9%; Pred. No. 38; ive 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SVIAKOMTYKVYMSGTV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 NVIKEFMRFKVRMEGTV 22
                                                                                                                                                                                                                                                            6 NVIKEFMRFKVRMEGTV 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SVIAKOMIYKVYMSGTV 17
                                                                                                                                                                                                                          1 SVIAKOMTYKVYMSGTV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 52,57
Best مربح 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Discosoma sp.
US-09-865-291-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Discosoma sp.
                                                                                       Query Match
Best Local Similarity 5
     ; TYPE: PRT
; ORGANISM: Discosoma sp.
US-09-794-308-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 12
LENGTH: 225
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Gaps

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Sequence 8, Application US/10081864

Publication No. US20030022287A1

GENERAL INFORMATION:

APPLICANT: Lukyanov, Sergey

APPLICANT: Lukyanov, Konstantin

APPLICANT: Lukyanov, Konstantin

APPLICANT: Savistky, Alexandr

APPLICANT: Savistky, Alexandr

APPLICANT: Savistky, Alexandr

APPLICANT: Savistky, Alexandr

TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and

TITLE OF INVENTION: No. US20030022287A2 Same

FILE REFERENCE: CLON-067

CURRENT APPLICATION NUMBER: US/10/081,864

CURRENT FLING DATE: 2001-12-04

PRIOR APPLICATION NUMBER: 10/066,922

PRIOR APPLICATION NUMBER: 60/270,983

PRIOR APPLICATION NUMBER: 60/270,983

PRIOR APPLICATION NUMBER: 60/270,983

PRIOR FILING DATE: 2001-02-21

NUMBER OF SEQ ID NOS: 30

SEQ ID NO 8

LENGTH: 225
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                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                               Query Match

48.2%; Score 40; DB 13; Length 225;
Best Local Similarity 52.9%; Pred. No. 38;
Matches 9; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 52.9%; Pred. No. 38;
Matches 9; Conservative 3; Mismatches 5; Indels
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 46
SOFTWARE: EsstSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: 225
                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: hybrid construct
US-10-006-922-44
                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVIAKOMTYKVYMSGTV 17
                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Discosoma sp.
US-10-081-864-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-081-864-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
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Gaps

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Search completed: August 12, 2004, 06:51:20 Job time : 35.7766 secs

| :|| : | :|| | ||| | 6 NVIKEFMRFKVRMEGTV 22 1 SVIAKOMTYKVYMSGTV 17

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 12, 2004, 06:12:47; Search time 1.77664 Seconds (without alignments) 493.990 Million cell updates/sec

Run on:

US-09-890-463-2 83 Perfect score: Sequence:

1 SVIAKOMTYKVYMSGTV 17

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 segs, 51625971 residues Searched:

389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptodata/2/iaa/5A COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Issued Patents AA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Segmence 43. Appl	Segmence 80. Appl	13,		Sequence 25. Appl	Sequence 13455. A	Sequence 4478. Ap			-		equence	m	m	21	42	9		검	5	23	23	23	23.	23,		2589
SUMMARIES	ID	-106-	US-09-106-568E-80	3-222-617A	US-08-222-617A-4	-08-222-	US-09-489-039A-13455	US-09-134-001C-4478	US-09-540-236-3211	US-09-540-236-2461	$\overline{}$	US-09-489-039A-13547	-101-60	US-08-446-692-3	US-08-488-351A-3	US-09-106-568E-21	US-09-100-409A-42	PCT-US95-13841-6	US-08-446-692-11	US-08-488-351A-11	US-09-134-000C-5981	US-08-292-968-23	US-08-467-974-23	-467-	-08	-09	US-09-106-568E-60	US-09-252-991A-25897
	DB	4	4	۲3	~	~	4	4	4	4	4	4	4	Н	~	4	٣	Ŋ	Н	7	4	~	7	7	m	m	4	4
	Length	107	107	3665	3712	3712	195	209	329	171	351	390	431	28	28	28	30	30	38	38	87	104	104	104	104	104	107	174
<b>0</b> *C	Query	51.8		47.0	47.0	47.0	45.8	45.8	45.2	44.6	44.6	43.4	43.4	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2
	Score	43	39	39	39	39	38	m	37.5	37	37	36	36						35									35
	Result No.	н	7	Э	4	2	ø	7	œ	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	26	27

Sequence 4, Appli	Sequence 4. Appli	52	No.	Patent No. 5223610	9	Sequence 7050. Ap	Sequence 14. Appl	2	Segmence 2. Appli	'n	,	471		Sequence 27, Appl			
US-08-849-376-4	PCT-US95-16450-4	5244657-9	5433945-9	5223610-9	US-08-836-236-6	US-09-107-532A-7050	US-09-491-577-14	US-08-142-439A-2	US-08-869-477-2	US-08-222-617A-5	US-09-177-650-3	US-09-328-352-4713	US-08-222-617A-12	US-08-222-617A-27	US-08-222-617A-2	US-09-328-352-4835	US-07-734-534A-5
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199	199	227	227	228	235	333	379	463	463	768	807	1085	3666	3727	3778	332	19
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42	42	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.2	41,6	41
35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	34.5	34
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

```
GENERAL INFORMATION:
APPLICANT: Bhattacharjee, J.
APPLICANT: Bhattacharjee, J.
APPLICANT: Bhattacherjee, Vasker
APPLICANT: Bhattacherjee, Vasker
ITILE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN
ITILE OF INVENTION: A BIOLOGICAL SAMPLE
FILE REFERENCE: 96,247-A
CURRENT APPLICATION NUMBER: US/09/106,568E
CURRENT FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: 08/650,809
PRIOR PAPLICATION NUMBER: 08/650,809
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 160
SOFTWARE MICROSOFT WORD 97
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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Patent No. 6455248
GENERAL INFORMATION:
APPLICANT: Bhattacharjee, J.
APPLICANT: Buvarna, Kalavati
APPLICANT: Bhattacherjee, Vasker
TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN
TITLE OF INVENTION: A BIOLOGICAL SAMPLE
FILE PERENCE: 96, 247-A
CURRENT APPLICATION NUMBER: US/09/106,568E
CURRENT PILING DATE: 1998-06-29
PRIOR PLING DATE: 1998-06-29
RECORD FRIENDER: 1997-05-20
NUMBER OF SEQ ID NOS: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Polypeptide segment of ACVS_EMENI shown in Figure 4. US-09-106-568E-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.8%; Score 43; DB 4; Length 107; 50.0%; Pred. No. 0.99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                        Sequence 43, Application US/09106568E Patent No. 6455248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVIAKOMTYKVYMSGT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |::||:| | ||||
1 SLTSKQLAYVTYTSGT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0°
Matches 8; Conservative
US-09-106-568E-43
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US-09-106-568E-80
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Length 3665;

us-09-890-463-2.rai

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Score 39; DB 2; I
Pred. No. 3.4e+02;
2; Mismatches 4;
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US-08-222-617A-25
Sequence 25, Application US/08222617A
Patent No. 582879
GENERAL INFORMATION:
HAPLICANT: Veenstra, Annemarie E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Veenstra, Annemarie E.
Martin, Juan F.
Garcia, Bruno D.
Gutierrez, Santiago
Barredo, Jose L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                           ; Sequence 4, Application US/08222617A; Patent No. 5882879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4:
      47.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 3712 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 SKOLAYVTYTSGT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AKOMTYKVYMSGT 16
                                                                                                                                                                           :||: | | |||
414 SKQLAYVTYTSGT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                   4 AKQMTYKVYMSGT 16
                                     Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 2555
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIALE. Chicago
STATE: Illinois
CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Veenst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-222-617A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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APPLICANT: Von Doehren, Hans
APPLICANT: Palisaa, Harriet
APPLICANT: Palisaa, Harriet
APPLICANT: Van Liempt, Henk
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: Amtibiotic Production and for Isolation of Large
TITLE OF INVENTION: Autibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of ACV Synthetase
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCDORNell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                      ; OTHER INFORMATION: Polypeptide segment of ACVS_CEPAC shown in Figure 4. US-09-106-568E-80
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= ACVS
/note= "ACV Synthetase from Acremonium
chrysogenum; aa 1-3665"
                                                                                                                                                                                                                                                                                                     47.0%; Score 39; DB 4; Length 107;
53.8%; Pred. No. 5.7;
tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-ARR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Acremonium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/0822617A
Patent No. 5882879
GENERAL INFORMATION:
APPLICANT: Veenstra, Annemarie E.
APPLICANT: Martin, Juan F.
APPLICANT: Garcia, Bruno D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martin, Juan F.
Garcia, Bruno D.
Gutierrez, Santiago
Barredo, Jose L.
Von Doehren, Hans
Palissa, Harriet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTER.FOTICS:
LENGTH: 3665 amino acids
STYPE: amino acids
STRANDEDNESS: single
                                                                                                                                             ORGANISM: Artificial sequence
                SOFTWARE: Microsoft Word 97
SEQ ID NO 80
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                            4 AKQMTYKVYMSGT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKOLAYVTYTSGT 16
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTY TO SET OF THE STATE OF SET OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NA ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                      TYPE: PRT
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APPLICANT: Palissa, Harriet
APPLICANT: Wan Liempt, Henk
APPLICANT: Wan Liempt, Henk
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of ACV Synthetase
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPPLICATION NUMBER: US/08/222,617A FILING DATE: 04-APR-1994 CLASSIFICATION: 435
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18-09-540-236-3211

Sequence 3211, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION
GENERAL INFORMATION:
TITLE OF INVENTION: NOTICEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARF
TITLE OF INVENTION: NOTICEIC ACID AND THERADEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERADEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERADEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2461, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GATY L.
Breton et al.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
                                                                                                                                           APPLICANT: LOS 03370
GENERAL INCORMATION:
APPLICANT: Lyan Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-.007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR PELING DATE: 1998-.08-13
PRIOR PILING DATE: 1997-111-08
PRIOR FILING DATE: 1997-114
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 209
LENGTH: 209
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Pred. No. 19;
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41.2%; Pred. No. 40;
                                                                                                       Sequence 4478, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OKGANISM: Staphylococcus epidermidis
US-09-134-001C-4478
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  86 VLEKOMISRGYMIG 99
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US-09-540-236-3211
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Best Local Similarity
7; Conserve
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Best Local Similarity
                                                                                     US-09-134-001C-4478
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Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: GARY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13455
LENGTH: 195
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APPLICANT: Garcia, Euno D.
APPLICANT: Gutierrez, Santiago
APPLICANT: Barredo, Jose L.
APPLICANT: Barredo, Jose L.
APPLICANT: Palissa, Harriet
APPLICANT: Palissa, Harriet
APPLICANT: Palissa, Harriet
APPLICANT: Van Liempt, Hank
APPLICANT: Wan Liempt, Hank
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                 ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: 111inois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
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Pred. No. 3.4e+02;
2; Mismatches 4
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Best Local Similarity 57.1%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 4
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ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 9'
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 3712 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.0%;
53.8%;
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Best Local Similarity 53.8*
T; Conservative
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                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell
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US-09-489-039A-13455
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Sequence 7056, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08446692
; Sequence 3, Application US/08446692
; Patent No. 575351
; GENERAL INFORMATION:
    APPLICANT: Ladd, Anna
    APPLICANT: Zamb, Timothy
    TITLE OF INVENTION: Immunogenic LHRH peptide constructs
    TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
    NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPAGE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-7un-1998
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 4;
Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature;
; LOCATION: (B) LOCATION 1...431
; SEQUENCE DESCRIPTION: SRQ ID NO: 7056:
US-09-107-532A-7056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                        ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 7056:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative 2
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US-09-107-532A-7056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-08-446-692-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999 CURRENT APPLICATION NUMBER: US/09/198,452A CURRENT FILING DATE: 1998-11-24 NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13547, Application US/09489039A

Sequence 13547, Application US/09489039A

Sequence 13547, Application US/09489039A

Sequence 13547, Application US/09489039A

Tutle OF INVENTION: VUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREUMONIAE POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1999-01-27

PRIOR PLING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 15547
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43.4%; Score 36; DB 4; Length 390;
Best Local Similarity 46.7%; Pred. No. 93;
Matches 7; Conservative 5; Mismatches 3: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 351;
                                                                                                                                Score 37; DB 4; Length 171; Pred. No. 23; 2; Indels
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Pred. No. 53;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 991, Application US/09198452A; Patent No. 6559294; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|: : |||:||
178 VAEFASQKVYVSGSV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.6%;
                                                                                                                                   Query Match

Best Local Similarity 63.6%;
Matches 7; Conservative
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64 LARGMIYKAIISNT 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.07
Best T, Conservative
                                                                                                                                                                                                                          QMTYKVYMSGT 16
                                                                                                                                                                                                                                                                      28 OKTYKVYINHT 38
                                             TYPE: PRT; ORGANISM: M.catarrhalis
US-09-540-236-2461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-489-039A-13547
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SEQ ID NO 2461
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US-08-488-351A-3
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Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESSEDNUBERS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                       CUMPIKY: US

CIP: 1014-0053

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US

ZIP: 10154-0053
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-UN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-UN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/29,275
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-446-692-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 KOMTYKVYMSG 15
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Best Local Similarity
Matches 5; Conserva
New York
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COUNTRY:
                                                  COUNTRY:
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APPLICANT: Bhattacharjee, J.
APPLICANT: Bhattacharjee, J.
APPLICANT: Suvarna, Kalavati
APPLICANT: Suvarna, Kalavati
APPLICANT: Bhattacherjee, Vasker
TITLE OF INVENTION: METHODS AND EAGENTS FOR DETECTING FUNGAL PATHOGENS IN
TITLE OF INVENTION: A BIOLOGICAL SAMPLE
FILE REFERENCE: 96.247-A
CURRENT APPLICATION NUMBER: US/09/106,568E
CURRENT FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: 08/650,809
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Microsoft Word 97
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:

CTHER INFORMATION: Polypeptide segment of ACVT_PENCH shown in Figure 4.
US-09-106-568E-21
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Pred. No. 6.8;
4; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.2%; Score 35; DB 4; 46.2%; Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                29,323
ER: 1151-4146 US2
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Job time : 2.77664 secs
APPLICATION NUMBER: US 08/057,166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-106-568B-21
; Sequence 21, Application US/09106568E
; Patent No. 6455248
                                                  ATTORNEY/AGENT INFORMATION:
NAME: MATIA C.H. Lin
REGISTRATION NUMBER: 1151
REPERENCE/DOCKET NUMBER: 1151
TELECOMUNICATION INFORMATION:
TELEPHONE: (512) 415-845
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                 42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial sequence
                     27-APR-1992
                                                                                                                                                                                                                                                                                                                                          4 AKQMTYKVYMSGT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.2
Matches 6; Conservative
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                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                               5 KOMTYKVYMSG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 RRLLYMIYMSG 14
                  FILING DATE: 27
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Colden) Mide of of shift

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein

Run on:

August 12, 2004, 06:12:47; Search time 21.3012 Seconds (without alignments) 1043.144 Million cell updates/sec

US-09-890-463-3 Title: Perfect score:

1268 1 SVIAKQMTYKVYMSGTVNGH.....SIARKPLVACCFFRVKSRHK 231 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues

Searched:

283366 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seq Minimum DB s Maximum DB s

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	green-fluorescent	probable membrane	hypothetical prote	organic solvent to	neural cell adhesi	anthranilate synth	hypothetical prote	E2 qlycoprotein pr	probable arylsulfa	reelin precursor -	alanyl-tRNA synthe	hynothetical prote	E2 glycoprofein pr	bable enzyme		colladen almba 2 c	hynothetical expor	probable photograt	ubiquinol-cytochro	CVSTPINE DIOLEGIAS	hypotherical prote	chlorophyll a/b-b;	probable transcrip	transcription sons	rohable transcript	hymothetical prote	donocurected process	linowmenage Atlow	lipoxygenase (EC 1
SUMMARIES	QI.	J01514	S64909	523818	E82323	IJMSNG	S00643	B70419	S14939	D64903	858870	A89944	358096	S14940	F90891	C85726	563985	D95982	T51828	B32382	S30149	S46636	CDPJ13	G65102	A91130	A85975	B64380	D69824	T47454	239
	DB	н	7	2	7	-	~	7				7	0	7						-	7	7		7	N	N	2	0	1 (1	7
	Query Match Length	238	583	752	787	725	770	260	1162	390	3461	876	248	1162	390	390	1822	334	403	687	363	1254	266	269	269	269	333	-	870	968
e)e	Query Match	4	8.4	7.1	6.9		6.8	6.3	•		•	•	6.5	٠	6.4	6.4	6.3	6.2	6.2	•	6.2	6.2	6.1	6.1	6.1	6.1	6.1		6.1	
	Score	184.5	106	06	ω	86.5	98	82	œ		83.5	•	82	m		81.5	80	79	79	7	•				77.5	77.5				
	Result No.	-1	7	ю	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

protein kinase (EC	xylulokinase homol	WD-40 repeat prote	chlorophyll a/b-bi	hypothetical profe	Dyruvate kinase (E	RNA-directed RNA n	El dlycoprofein -	alpha-1-B-dlycopro	hynothetical prote	hypothetical prote	hypothetical prote	denome nolvorotein	structural polypro	chlorophyll a/h-h-i	32.3K hypothetical
T14050	E69895	AC2239	CDPJ25	E65045	826869	P2IVBS	A48608	A42013	T24593	E71425	G71175	S26373	S72350	CDPJZL	B86370
7	7	7	Н	~	~	н	~	~	~	7	N	7	7	Н	7
1702	487	1526	566	444	526	725	207	237	275	297	438	1241	1242	267	276
6.1	6.1	6.0	0.9	6.0	0.9	6.0	0.9	0.9	6.0	0.9	6.0	6.0	0.9	5.9	5.9
77.5	77	76.5	94	92	92	16	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75	75
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

A;Cross-references: GB:L29345; NID:g606383; PIDN:AAA58246.1; PID:g606384 R;Watkins, J.N.; Campbell, A.K. submitted to the EMBL Data Library, January 1995 A;Reference number: S51330 A;Accession: S51330

A.Molecule type: mRNA A.Residues: 1-13,'V',15-24,'Q',26-44,'N',46-153,'G',155-156,'P',158-171,'K',173-227,'R',; A.Cross-references: EMBL:X83959; NID:g634008; PIDN:CAA58789.1; PID:g634009 A.Experimental source: clone gfp1

A;Accession: S5131
A;Molecule type: mRNA
A;Residues: 1-24, Q', 26-29, R',31-83, 'L',85-153, 'G',155-156,'P',158-171,'K',173-208,'Q',;
A;Cross-references: EMBL:X83960; NID:g634010; PIDN:CAAS8790.1; PID:g634011
A;Experimental source: clone gfp2
R;Yang, F.; Moss, L.G.; Phillips Jr., G.N.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A65692; PDB:LGFL

A.Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 'A',2-79,'R', 81-95 A.Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 'A',2-79,'R', 81-95 A.Note: engineered sequence based on JQ1514, cloned and expressed in Escherichia coli R;Yang, F; Moss, LG.; Phillips Jr., G.N.
Nat. Biotechnol. 14, 1246-1251, 1996
A;Title: The molecular structure of green fluorescent protein.
A;Reference number: A58953; MUID:98294543; PMID:9631087

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organic solvent tolerance protein VC0446 [imported] - Vibrio cholerae (strain N16961 ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A62035; MJID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE004131; GB:AE003852; NID:g9654856; PIDN:AAF93619.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: E82323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.3;
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                                                                                                                      583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.1%; Score 90;
23.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Mobile element: transposable element Taml
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                                                      200 NKDYTSVEOREISIARKPLVACCFFRV
                                                                                                   SKLHLKKEORVVTNGNK---SCLYWRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: X57297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 29-752 < NAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-787 <HEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: S16551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Start codon: GTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S:
Matches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31
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                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
S64909
N;Alternate names: hypothetical protein L2349
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Ol-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2002
C;Accession: S64909
R;Pohl, T.M.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64899
A;Reference number: S64899
A;Rocession: S64909
A;Rocession: 
A;Contents: annotation; X-ray crystallography, 1.9 angstroms
C;Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittin
C;Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-
C;Genetics:
A;Gene: GFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 NNQLFEIELLNKFK-HEGEDVVRKREIKKIACGSYHTLAIDKTGEIYAFGWN-----RF 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            402 GOLALPISYNLEYVSFPRSVTHAFKPHFPGMTNWKCVDIHCDDETSFVTIRKPGSTSDHH 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEDIP--DYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVMQKKTQGWEPNTERLF----ARDGMLIGNNF-MALKLEGGGHYLCEF--KSTYKARK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFTKY 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462 YFAFGNGLFGELGNNTFKNSQCDPIKIKSD------DKKLTNWSCGSHCVFTETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 VELDGDVNGHKESVSGEGEGDATYGKLTLKFICTT-GKLPVPWPTLVTTFSYGVQCFSRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAVTKGGPL-PFAWDILSPQCQY
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                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                             A;Introns: 69/3; 167/3
C;Superfamily: green-fluorescent protein
C;Superfamily: green-fluorescent protein
C;Keywords: chromoprotein; luminescence
E;65-67/Cross-link: 5-imidazolinone (Ser-Gly) #status experimental
F;66/Modified site: dehydrotyrosine (Tyr) #status experimental
                                                                                                                                                                                                                                                                                                                                              Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
8.4%; Score 106; DB 2; Length 583;
Best Local Similarity 21.0%; Pred. No. 0.18;
Matches 56; Conservative 33; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
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                                                                                                                                                                                                                                                                                                                                              14.6%; Score 184.5; DB 1
llarity 24.8%; Pred. No. 6.4e-09;
Conservative 47; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | : | | | : : : | : | : | : | PVLLPDNHYLSTQSALSKDPNEKRDH 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 PVKMPGYHYVDRKLDVT---NHNKDY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 NGHYFEVEGDGKGKPYEGEQTVR
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 51;
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Best Local S:
Matches 51
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A;Residues: 1-722 cARC.
A;Cross-references: EMBL:X57297
R;Nacken, W.K.F.; Piotrowiak, R.; Saedler, H.; Sommer, H.
Rol. Gen. Genet. 228, 201-208, 1991
A;Title: The transposable element Taml from Antirrhinum majus shows structural homology
A;Reference number: S16551; MUID:91360065; PMID:1715971
                                                                                                                                                                                                                                                  hypothetical protein Tnp2 - garden snapdragon transposable element Taml hypothetical protein Tnp2 - garden snapdragon) c;Species: Antirrhinum majus (garden snapdragon) c;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Sep-1998 C;Accession: S23818; S16551 R;Nacken, W.K.F.; Piotrowiak, R.; Saedler, H.; Sommer, H. submitted to the EMBL Data Library, January 1991 A;Description: The transposable element TAM1 from Antirrhinum majus shows structural PA;Reference number: S23817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         530
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559
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--DHGQLGIGKKTMKCAKPMNIPEVLKPGQDTTD--LDSIYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---RKPLV-ACCFFR 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 IMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPN----
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           511 QENEVIAWGNN-
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us-09-890-463-3.rpr

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A;Gene: trpC
C;Superfamily: trpG-trpC-trpF trifunctional enzyme; trpC homology; trpF homology; trpG hc
C;Keywords: carbon-carbon lyase; carboxy-lyase; intramolecular lyase; isomerase; oxo-acic
F;25-219/Domain: glutamine amidotransferase #status predicted <GAT>
F;26-216/Domain: trpG homology <TRG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Aspergillus niger
C;Date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text_change 31-Mar-2000
C;Dates: 07-Sep-1990 #sequence revision 07-Sep-1990 #text_change 31-Mar-2000
C;Accession: 800643; A32979; B32979
R;Kos, T.; Kuijvenhoven, A.; Hessing, H.G.M.; Pouwels, P.H.; van den Hondel, C.A.M.J.J.
Curr. Genet. 13, 137-144, 1988
A;Title: Nucleotide sequence of the Aspergillus niger trpC gene: structural relationship
A;Reference number: 800643; MUID:88223483; PMID:2836085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X07071; NID:g2420; PIDN:CAA30107.1; PID:g2421
R;Kos, A.; Kuijvenhoven, J.; Wernars, K.; Bos, C.J.; van den Broek, H.W.J.; Pouwels, P.H.
Gene 39, 231-238, 1985
A;Reference number: A91539; MUID:86137391; PMID:2936650
F;625-685/Domain: fibronectin type III repeat homology <FN3B>
F;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F;222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anthranilate synthase multifunctional protein - Aspergillus niger
N;Alternate names: gene trpG-trpC-trpF protein; glutamine amidotransferase
N;Contains: anthranilate synthase (EC 4.1.3.27); indole-3-glycerol-phosphate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F:255-518/Domain: trpC homology <TRC>
F:255-518/Domain: indole-3-glycerol-phosphate synthase #status predicted <IGPS>
F:537-767/Domain: trpF homology <TRF>
F:537-770/Domain: N-(5'.phosphoribosyl)anthranilate isomerase #status predicted <PRAI>
F:104/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                     ----QCQY-----GSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSI 108
                                                                                                                                                                                                                                                                                                                                   455 KIY--NTPSASYLEVTPDSENDFGNYNCTAVNRIGOESLEFILVQADTPSSPSIDRVEPY 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 QGNCFI-----YHVKFSGLNFPPNGPVMQ---KKTQG----WEPNTERLFARDGMLI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             619 KVNL--IKQDDGGSPIRHYLVKYRALASEWKPEIRLPSGSHHVMLKSLDWNAEYEVYVVA 676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 GNNFMALKLEGGG----HYLCEFKSTYKARKP-VKMP--GYHYVDRKLDVTNHNKDYTSV
                                                                                                                                                                                                                                                                    10 KVYMSGIVNGHYFEVEGDGKGK--PYE-----GEQTVR-LAVTKGGPLPFAWDILSP-
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A,Residues: 1-69 <KO2>
A,Cross-references: GB:M14404; NID:g166536; PIDN:AAA32709.1; PID:g166537
A,Accession: B23979
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A;Residues: 392-433 <KO3>
A;Cross-references: GB:M14403; NID:g166538; PIDN:AAA32710.1; PID:g166539
                                                                                                                                                                                                         61;
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                                                                                                                                       Length 725;
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                                                                                                                                                                                                         Indels
                                                                                                                                                                                                         . 68
                                                                                                                                       DB 1;
                                                                                                                                6.8%; Score 86.5; DE 21.7%; Pred. No. 12; ative 41; Mismatches
                                                                                                                                                                                                      Conservative
                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-770 <KOS>
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Matches
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C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 31-Dec-2000
C;Accession: A22673; S00382; A44290
R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000
A;Reference number: A29673; MUID:87246524; PMID:3595563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol C: Comment: Several forms of NCAM are produced by alternative splicing. See also PIR: 1JMG C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JINITORS: 701/1
;Superfamily: neural cell adhesion molecule, fibronectin type III repeat homology, immu
;Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane
;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
R.Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
R.Barbo J. 7, 625-632, 1988
A.Title: Differential splicing and alternative polyadenylation generates distinct NCAM A; Reference number: S00382; MUID:88283628; PMID:3396534
A; Accession: S00382
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A,Residues: 642-656, D',658-725 <BA2>
A,Cross-references: EMBLX07195
R,Rougon, G; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A,Title: Structural and immunological characterization of the amino-terminal domain of
A,Reference number: A44290; MUID:86140120; PMID:3512556
                                                                                                                                                                                               9;
                                                                                                                                                                                                                                                                                                                                                                                    57 SPQCQYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYH 116
                                                                                                                                                                                                                                                                                                                                   443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480
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                                                                                                                                                                                                                                                       6 QMTYKVYMSGTVN-----GHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFA--WDIL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 VKFSGLNFPPNGPVMQKKTQGWEPNTERLFA------RDGMLIGNNFWAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 QLSYNYYAPETMKYLDLDLVSHVSRFETDARGKP----SATRVHIEPGLKIPFSNTWGNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                             --AKLEESVTRVIPEIRSV------
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 ----KLEGG-----GHYLCEFKSTYKARKPVKMPGYHYVDRKLDVTNHNKDYTS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGVDRIESANQVSYGASTRFFDSNYKERLNIAFGQIFYLDSKLNPSNKNPDSTS 591
                                                                                                                                                                                           64;
                                                                                                               Query Match 6.9%; Score 87; DB 2; Length 787; Best Local Similarity 19.2%; Pred. No. 12; Matches 45; Conservative 33; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;228-290/Domain: immunoglobulin homology <inMu3>
F;228-272/Region: NCAM binding #status predicted
F;323-388/Domain: immunoglobulin homology <inMu4>
F;420-482/Domain: immunoglobulin homology <inMu4>
F;519-596/Domain: fibronectin type III repeat homology <FN3A>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
             A;Map position: 1
C;Superfamily: organic solvent tolerance protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34-98/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  444 TTEAR---VLGTYYQQDLDKTTD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 20-36 < ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-725 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A29673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A44290
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Best Local Similarity   21.1%;   Pred. No. 37;   Redels   134;   Gaps   17;	THY THE TINNGLWENS TO STATE THE TOTAL TOTAL THE TOTAL	RESULT 9 D64903 D64903 D64904 Drobable arylsulfatase activating enzyme (EC 1) b1497 [similarity] - Escherichia cc C; Species: Escherichia coli C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002 C; Accession: D64903 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col. Science 277, 1452-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: D64903 A;Status: nucleic acid sequence not shown; translation not shown A; Date: 12-30, A1AAT, A; Desidner: 1-300, A1AAT,	A; cross-references: GB1.AE000247; GB:U00096; NID:g1787773; PIDN:AAC74570.1; PID:g1787774; A; Experimental source: strain K-12, substrain MG1655 C; Genetics: A; Start codon: TTG C; Superfamily: arylsulfatase activating enzyme atsB C; Superfamily: arylsulfatase activating enzyme atsB C; Keywords: oxidoreductase C; Keywords: oxidoreductase 6.6%; Score 83.5; DB 2; Length 390; Best Local Similarity 19.6%; Pred. No. 10; Matches 55; Conservative 46; Mismatches 104; Indels 75; Gaps 12;	QY         10 KVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAV-TKGGFLPF 51           Db         49 KQYIAASGNQVYFTWQGGEPTLAGLDFFRKVIHYQQRYAGQKRIFNALQTNGILLNN 105           QY         52 AWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFE-DGAVCTVS 103           Db         106 EWCAPLKEHFFLVGISIDGPQELHDRYRKSNGGNGTFAKVIAAIERLKSYQVEFNTLTVI 165	104 166 130 226 187 281 281 8870
Db 117 KVDVTGEILHGKTSPLKHDGKG-AYEG	RESULT 7 B70419 hypothetical protein ag 1369 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Dace: 08-May-1998 #sequence_revision 08-May-1998 #text_change 04-Mar-2000 C;Accession: B70419 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov	53-358, 1998  complete genome of the hyperthe under: A70300; MUID:98196666; PB70419  liminary; nucleic acid sequence ppe: DMA  ppe: DMA  ppe: DMA  acces: GB-AE000737; NID:9298378  l source: strain VF5  69  condition acolicus hypothetical  Aquifex acolicus hypothetical			riby r-1997 #text_change 31-Oct-19 I.M.; Zijderveld, A.J.; Bleum M41 strain of coronavirus I M1D:2429473 not shown  DB 2; Length 1162;

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A;Cross-references: EMBL:Z50112; PIDN:CAA90455.1; GSPDB:GN00066; SPDB:SPAC13C5.04
A;Experimental source: strain 972h-; cosmid c13C5
C;Genetics:
                             11;
                                                                                                                                                                                                                     --FAWEFLTSDKWMGMEPDKLYVTIH 130
                                                                                                                                                                                                                                                                                                                                                                                              131 PEDMEAY------NIWHKDIGLEESRII-----RIEGN-----FWDIGEGPSG-- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 MOKKTOGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARKPVKMPGYHYV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 KYPEDIPDYVKQSFPGRYTWERIMN--FEDGAVCTVSND-----SSIQGNCFIY-HV 117
                                                                                                                            70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 KNPNDYPQ--KEDFPN-----INAIIITGSKASATSDAPWIKKLISFVKDVLFKYPHI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -PNTERLFARDGMLIG--NNFMA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 LKLEGGGHYL-----CEFKSTYKARKPVKMPGY-----HYVDRKLDVTNHNKDYTSVEQR 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: | :: | :: | :: |: | :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: |: :| :: :| :: |: :| :: |: :| :: :| :: |: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein SPAC13C5.04 - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Date: i3-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91ycoprotein precursor - avian infectious bronchitis virus (strain M42-S)
                                                                                                                                                                                                                                                                                                          71 PEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPV
                                                                                                             16 TVNGH-YFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIP----FTKY
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:250112; NID:9908889; PIDN:CAA90455.1; PID:9908893 R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, July 1995
                             79;
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                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PNTEIFYDR-GEAYGODDPAEEMYPGGEN---
                             60;
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CySpecies: avian infectious bronchitis virus, IBV
A,Variety: strain M42-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| |:|
196 ERYLEVWNLVFSEFNHNKDHSYTPLPNKNI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 DRKLDV-----TNHNKD--YTSVEOREI 211
                             25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 KFSGLNF-----PPNGPVMQKKTQGWE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, July 1995
A;Reference number: S58093
                                                                                                                                                                                                                81 TARHHTFFEMLGNFSIGDYFKOEAIE-
                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Matches 45; Conserv
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A,Status: preliminary
A,Molecule type: DNA
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              46;
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E2 glycopr
                   Matches
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                        C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 21-Jul-2003
C.Date: 06-Dec-1996 #text_change 21-Jul-2003
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-Mar-2003
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-Mar-2003
C;Accession: A8994
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2080 YYAĞITQĞWRREVVHFĞKLHLCĞ-----SVRFRWYQĞFYPAĞSQPVTWAİDNVYIGPQ 2132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2193 RKCGILSSGNNLFFNEDGLRMLVTRDLDLS-----HARFVQFFMRLGCGKGVPDPRSQP 2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Molecule type: mRNA
A;Residues: 1-215, T', 217-1905, S',1907-3355, VV, 3357-3391, NV, 3393-3461 <DA2>
A;Cross-references: EMBL:U24703; NID:g902486; PID:g902487
F;1-27/Domain: signal sequence #tatus predicted <SIG>
F;28-3461/Product: reelin #status predicted <MAT>
F;1769-1795/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDGAVCTVSNDSSIQGNCFIYHVKF-----SGLNFPPNGP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- QKKTQGWEPNTERLF--- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Residues: 1-876 <KUR>
A)Cross-references: GB:BA000018; PID:g13701416; PIDN:BAB42710.1; GSPDB:GN00149
A)Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 YMSGTVNGHYFEVEGDGK----GKPYEGEQTVRLAVTKG----GPLPFAWDI----LSPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SIPFTKYPEDIPDYVKQSFPGRYTWERIMNF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75; Indels 125;
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Pred. No. 1.6e+02;
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submitted to the EMBL Data Library, April 1995
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C,Superfamily: alanyl-tRNA ligase
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nes 57, Conservative
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reelin precursor - mouse
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Cipate: 18-701-2001 #sequence_revision 18-701-2001 #text_change 03-Aug-2001

Cipate: 18-701-2001 #sequence_revision 18-701-2001 #text_change 03-Aug-2001

Cipate: 18-701-2001 #sequence_revision 18-701-2001 #tipate 1: Hattori, M.; Yokoyama, K.; Han, C.G.

Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DAN Res, 8, 11-22, 2001

A; Fitte: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gency

A; Reference number: A99629; MUID:21156231; PMID:11258796

A; Accession: F90891

A; Status: preliminary

A; Residues: 1-390 *HAY>

A; Experimental source: Strain 0157:H7, substrain RIMD 0509952
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C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C; Accession: S14940
R; Niesters, H.G.M.; Lenstra, J.A.; Spaan, W.J.M.; Zijderveld, A.J.; Bleumink-Pluym, I Virus Res. 5, 253-263, 1986
A; Title: The peplomer protein sequence of the M41 strain of coronavirus IBV and its capacession: S14940
A; Accession: S14940
A; Acc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --VKFSG------LNFPPN--GP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 PDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNC----FIYHVKFSGLNFPPNG-- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --PVMQKKT-QGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARKPVKMP 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65; Indels 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 NIQTYQTKTAQSGYYNFNFSFLSSFVYKESNFM----YGSYHPSCNF---
                                                                                                                                                                                                                                                                                                                                                                                                            6.5%; Score 82; DB 2; Length 1162; 20.7%; Pred. No. 55; ive 29; Mismatches 65; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 VAKYPTERSFQCVNNLTSVYLNGDLVYTSNETIDVTSAGVYFKA--
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C;Superfamily: arylsulfatase activating enzyme atsB
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nes 60; Conservative
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probable enzyme Z2211 [imported] - Escherichia coli (strain O157:H7, substrain EDL933) C;Species: Escherichia coli (c;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: C85726 E. 17. Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Feference number: A885480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-390 <STO>
A;Cross-references: GB:AE005174; NID:g12515177; PIDN:AAG56271.1; GSPDB:GN00145; UWGP:Z227
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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130 VMQKKTQGWEPN-TERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARKPVKMPG-- 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -YEGEQTVRLAV-TKGGPLPF.
                                                             226 FMSTIFMQWVKNDVGEIFIRQFESFVSRFL----GNGHTSCIFQESCKDNLVVESNGDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:| : : : | | | 281 YECDHFVYPQYKLGNINKSELKTMNSVQLTAQKKRISAKC 320
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                                                                                                                                        ---YHYVDRKLDVTNHNK-DYTSVEOREISIARKPLVACC 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 NDSSIQGNCFIYH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: C85726
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

August 12, 2004, 06:12:47; Search time 14.2008 Seconds (without alignments) 847.008 Million cell updates/sec

US-09-890-463-3 1268 1 SVIAKQMTYKVYMSGTVNGH.....SIARKPLVACCFFRVKSRHK 231 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	1	Description	2 aequorea vi	vibrio cl				avian ir		1 mus musculu	1 staphylococ				ᅺ		ď	1 bradyrhîzob			•		_	7 buchnera ap	bacillus	-		1 anabaena sp			6 influenza b	0 homo sapien		4	6 caldocellum
co.	·	Descr	P42213	Z9kur	P13594	P05328	067381	P11223	P76134	Q60841	Q99tn	Q8nw8	989600	P5875	Q9nrm1	P1358	082660	P51131	09ers7	P39538	P04779	P42902	Q58059	Q8k9a	P5460	P38418	036432	Q8yri1	P0478	P3733	P1113	Ondn60	P04780	S	P2355
SUMMARIES	Ę	i	GFP_AEQVI	OSTA_VIBCH	NCA2 MOUSE	TRPG ASPNG	YD69 AQUAE	VGL2_IBVB	YDEM_ECOLI		SYA_STAAM		YA14 SCHPO	RELN RAT	ENAM_HUMAN	ATA1_CHICK	H136_ARATH	CYBC_BRAJA	IRL2 MOUSE	UBPC_YEAST	CB21 PETSP	AGAR_ECOLI	Y642 METJA	MLTA_BUCAP	YHCX_BACSU	LOXC_ARATH	RRP2_INBP9	YY46_ANASP	CB24_PETSP	YGAF_ECOLI	RRP2_INBSI	TF20_HUMAN		YF99 METJA	XYNA_CALSA
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÷	Query		14.8	6.9	6.8	6.8	6.7	9.9	9.9	9.9	6.5	6.5	9 1	6.4	4.1	6.3	6.2	6.2	6.2	6.2	6.1	6.1	6.1	6.1	6.1	6.1	6.1	0.9	0.9	0.9	0.9	0.9	υ i	υ. ο.	ر. ي.
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Q02219 neisseria g Q8pce0 xanthomonas Q9epq8 mus musculu P36310 parvovirus	015020 homo sapien P07370 lycopersico	P04783 petunia sp. P55631 rhizobium s P23772 mus musculu	Q8pp22 xanthomonas Q8csa7 staphylococ P23249 mus musculu
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34 35 37	8 8 8	441	4 4 4 5 4 5

## ALIGNMENTS

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71 PEDIP---DYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 VYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.8%; Score 187.5; DB 1; Length 238; 25.2%; Pred. No. 9.5e-10; ive 46; Mismatches 91; Indels 17;
                                                                                                                                                                                                                                                                                    5-imidazolinone (Ser-Gly).
2,3-DIDEHYDROTYROSINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26886 MW; EASAGF21FBFB6E05 CRC64;
                                                                                                                                                                                                              PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
Luminescence; 3D-structure.
                                                                                                                  PDB; ZEMO; Z0-AUG-97.
Interpro; IPR009017; GFP_like.
Interpro; IPR000786; Green_fl_protein.
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Best Local Similarity 25.2'
Matches 52; Conservative
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                      10-APR-02.
28-OCT-98.
20-AUG-97.
                                                                                              20-AUG-97
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PDB; 1KYR; 1
PDB; 1KYS; 1
PDB; 1YFP; 2
PDB; 2EMD; 2
PDB; 2EMN; 2
PDB; 2EMN; 2
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PINSOLE STELLITIES INCOCYTEES.

OF modified an active actives. The chromophore is formed upon cyclication of the residues. The chromophore is formed upon cyclication of the residues Ser-dehydroTyv-Gly.

BIOTECHNOLOGY: Has become a useful and ubsiquitous tool for making chimeric proteins of GFP linked to other proteins tool for making functions as a fluorescent protein tag. GFP tolerates N-and C-terminal fusion to a broad variety of proteins. It has been expressed in bacteria, yeast, slime mold, plants, prosophila, zebrafish, and in mammalan cells. As a noninvasive fluorescent marker in living cells, it allows for a wide range of applications where it may function as a cell lineage tracer, reporter of gene
                                                                                                                                                                                                                   [7]

**RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION.

**MEDLINE=98455509; PubMed=9782051; Mallio K., Hanson G.T., Remington S.J.; Machter R.M., Elsilger M.A., Kallio K., Hanson G.T., Remington S.J.; "Structural basis of spectral shifts in the yellow-emission variants of green fluorescent protein.";

**Structure 6:1267-1277(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression, or as a measure of protein-protein interactions. DATABASE: NAME-Protein Spotlight;
NOTE-Issue 11 of June 2001;
WWW="http://www.expasy.org/spotlight/articles/sptlt011.html".
                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: Photocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M62654; AAA27722.1; -.
EMBL; M62653; AAA27721.1; -.
EMBL; L29345; AAA58246.1; -.
EMBL; X96418; CAA65278.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . JS0692; JQ1514.
; IB9C; 17-NOV-00.
; IBFP; 07-JUL-97.
; IC4F; 14-JUN-00.
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20-AUG-97.
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129 PVMQKKTQGWEPNTERLF----ARDGMLIGNNF-MALKLEGGGHYLCEF--KSTYKARK 180

20

Gaps

17;

PVKMPGYHYVDRKLDVT---NHNKDY 203

181

à 임 ò

11-JAN-97

1HCJ;

1EML;

1EMA; 1EMB;

1EMC; 1EMF; 1EMG;

1KP5; 1KYP;

us-09-890-463-3.rsp

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192 PVLLPDNHYLSTQSALSKDPNEKRDH 217

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 VKFSGLNFPPNGPVMQKKTQGWEPNTERLFA------RDGMLIGNNFMAL----- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 ---AGIVLERDIVLLDDYİQILEPKIQYLYVPEKYQDNIGLYDSTLLQIDYYGLFRSRKY 537
                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 406 477-483 (2000).
-!- FUNCTION: Determines N-hexane tolerance. Involved in outer membrane permeability. Essential for envelope biogenesis. Could be part of a targeting/usher system for outer membrane components (By
                                                                                                                                                                                                                                                                MEDLINE=20406833; PubMed=10552301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Oin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 QMTYKVYMSGTVN-----GHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFA--WDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388 QLSYNYYAPPETMKYLDLDLVSHVSRFETDARGKP----SATRVHIEPGLKIPFSNTWGNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444 TTEAR---VLGTYYQQDLDKTTD------AKLEESVTRVIPEIRSV----
                                                                                                                                                                                                                                                                                                                                                                                                         "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANIC SOLVENT TOLERANCE PROTEIN; 036718F1896E0F7D CRC64;
                                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.9%; Score 87; DB 1; Length 787; Best Local Similarity 19.2%; Pred. No. 4.4; Matches 45; Conservative 33; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Outer membrane (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Organic solvent tolerance protein precursor.
IMP OR OSTA OR VC0446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33; Mismatches
                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-El Tor N16961 / Serotype Ol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE004131; AAF93619.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89017 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                  STANDARD;
                                                                                                                                                                              Vibrionaceae; Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; E82323; E82323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   787 AA;
                                                                                                                                         Vibrio cholerae.
                                                                                                                                                                                               NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity)
                VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
OSTA_VIBCH
ID OSTA_VIB
AC Q9KUR9;
                                                                                                                                                                                                                                                                                                                                                                                                                               cholerae
                                                                                                                                                                                                                                                                                                                                                                                            Fraser
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                                                                                                                                                                                       01-07N-1990 (Rel. 13, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Neural cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6; IISSUE=Brain; MEDLINE=89251563; PubMed=2721486; Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille M.; "Differential exon usage involving an unusual splicing mechanism generates at least eight types of NCAM cDNA in mouse brain."; EMBO J. 8:385-392(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barthels D., Santoni M.-J., Wille W., Ruppert C., Caix J.-C.,
Hirsch M.-R., Fontecilla-Camps J.-C., Goridis C.,
"Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
a Mr 79,000 polypeptide without a mewbrane-spanning region.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=86140120; PubMed=3512556;
Rougon G., Marshak D.R.;
"Structural and immunological characterization of the amino-terminal
161 ----KLEGG-----GHYLCEPKSTYKARKPVKMPGYHYVDRKLDVTNHNKDYTS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurites, etc.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.; "Differential splicing and alternative polyadenylation generates distinct NCAM transcripts and proteins in the mouse.";
                        538 SGVDRIESANQVSYGASTRFFDSNYKERLNIAFGQIFYLDSKLNPSNKNPDSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: This protein is a cell adhesion molecule involved neuron-neuron adhesion, neurite fasciculation, outgrowth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 261:3396-3401(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain of mammalian neural cell adhesion molecules.";
                                                                                                                                    725 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P13594-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P13595-1; Sequence=External;
Name=N-CAM 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lsoId=P13595-2; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88283628; PubMed=3396534;
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87246524; PubMed=3595563;
                                                                                                                                NCA2_MOUSE STANDARD;
P13594; Q61950;
01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 642-725 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 20-700 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBO J. 6:907-914 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 7:625-632(1988)
                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6;
                                                                                                                                                                                                                                                      (NCAM-120).
NCAM1 OR NCAM.
                                                                                                                  NCA2_MOUSE
                                                                                             RESULT 3
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455 KIY--NTPSASYLEVTPDSENDFGNYNCTAVNRIGQESLEFILVQADTPSSPSIDRVEPY 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 GNNFMALKLEGGG----HYLCEFKSTYKARKP-VKMP--GYHYVDRKLDVTNHNKDYTSV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          619 KVNL--IKODDGGSPIRHYLVKYRALASEWKPEIRLPSGSHHVMLKSLDWNAEYEVYVVA 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----QCQY-----GSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 KVYMSGTVNGHYFEVEGDGKGK--PYE-----GEQTVR-LAVTKGGPLPFAWDILSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---YHVKFSGLNFPPNGPVMQ---KKTQG----WEPNTERLFARDGMLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 559 EGIVTÍMGLKPETTÝSDRLAALNGKGLGEIMQPSESKTQPVPELSAPKLEGQMGEDGNSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89; Indels 61; Gaps
                                                                                                                                                                                                                                NEURAL CELL ADHESION MOLECULE 1, 120 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAN
N-LINKED (GLCNAC. . .) (POTENTIAN
ERSESSOYS -> DEKHIFSD (IN REF. 2)
V -> L (IN REF. 2).
QD -> KT (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%; Score 86.5; DB 1; Length 725; 21.7%; Pred. No. 4.4; ive 41; Mismatches 89; Indels 6:
                                                                                                                                                     SMARY; SM0006); FN3; 2.
SMARY; SM00408; IGC2; 5.
SMARY; SS00815; IG_LIKE; 5.
Cell adhesion; Glycoptcein; Repeat; Alternative splicing; Immunoglobulin domain; Signal; Heparin-binding; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T -> K (IN REF. 2).
T -> R (IN REF. 2).
D -> V (IN REF. 2).
MQPES -> SAATEF (IN REF. 2).
PEL -> REP (IN REF. 2).
H -> D (IN REF. 2).
W; CZAEB8B4461C6B2F CRC64;
                                                                                                                                                                                                                                                                                                                                     HEPARIN-BINDING (POTENTIAL).
HEPARIN-BINDING (POTENTIAL).
                                                                                                                                                                                                                                           ISOFORM.

1G-LIKE C2-TYPE 1.

1G-LIKE C2-TYPE 2.

1G-LIKE C2-TYPE 4.

1G-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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T -> K (IN
T -> R (IN
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                                                                        MGD; MGI:97281; Ncam:
InterPro; IPR008957; FN_III-like.
InterPro; IPR003961; FN_III.
InterPro; IPR007110; Ig-like.
InterPro; IPR005598; Ig_c2.
Pfam; PF00041; fn3; 2.
Pfam; PF00047; ig; 5.
        EMBL; Y00051; CAA68263.1; -.
EMBL; X15049; CAA33148.1; ALT_SEQ.
EMBL; X07195; CAA30173.1; -.
EMBL; A29673, LJMSNG.
PDB; 2NCM; 12-MAR-97.
PDB; 3NCM; 23-UUL-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80296 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 21.7
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 288
388
3386
3316
3316
4424
4450
2273
3355
5449
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2005
3002
3002
4402
6902
6902
1165
96
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657
725 AA;
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222
316
316
424
450
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273
354
549
572
589
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SIGNAL
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DOMAIN
DISULFID
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CARBOHYD
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Best Local
                                                                                                                                                                                                                                                                                                                                                                      DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 39:231-238 (1985).

- I- FUNCTION: TRIFFUNCTIONL ENZYME BEARING THE GLN AMIDOTRANSFERASE

- GATASED, DOWAIN OF ANTHRAULATE SYNTHASE, INDOLE-GLYCEROLPHOSPHATE

SYNTHASE, AND PHOSPHORIBOSYLANTHRANILATE ISOMERASE ACTIVITIES.

- CATALYTIC ACTIVITY: N. (5-phospho-beta-0-ribosyl) -anthranilate = 1-

- CATALYTIC ACTIVITY: 1-(2-arboxyphenylamino) -1-deoxy-D-ribulose 5-phosphate = 1-(indol-3-yl)glycerol 3-phosphate + CO(2) + H(2)O.

- CATALYTIC ACTIVITY: (Cariborate + L-glutamine = anthranilate + pyruvate + L-glutamate.

- CATALYTIC ACTIVITY: Chorismate + L-glutamine = anthranilate + pyruvate + L-glutamate.

- PATHWAY: Tryptophan biosynthesis; first step.

- PATHWAY: Tryptophan biosynthesis; fourth step.

- PATHWAY: Tryptophan biosynthesis; fourth step.

- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECURINCE OF 1-69 AND 392-433 FROM N.A.
MEDLINE=86137391; PubMed=2936650;
Kos A., Kuijvenhoven J., Wernars K., Bos C.J., van den Broek H.W.J.,
Powwels P.H., van den Hondel C.A.M.J.J.;
"Isolation and characterization of the Aspergillus niger trpC gene.";
                                                                                                                                                                             01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Anthranilate synthase component II (EC 4.1.3.27) [Includes: Glutamine amidotransferase; IndoLe-3-glycerol phosphate synthase (EC 4.1.1.48)
(IGPS); N-(5'-phosphoribosyl)anthranilate isomerase (EC 5.3.1.24)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Nucleotide sequence of the Aspergillus niger trpC gene: structural relationship with analogous genes of other organisms."; Curr. Genet. 13:137-144(1988).
                                                                                                                                                                                                                                                                                                                    Aspergillus niger.
Bukaryota; Pungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88223483; PubMed=2836085;
Kos T., Kuijvenhoven A., Hessing H.G.M., Pouwels P.H.,
van den Hondel C.A.M.J.J.;
                                                                                                                                         ¥
                                                                                                                                         770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006220; Anth synthII.
InterPro; IPR001301; CP_synthGATase.
InterPro; IPR0013009; FNN enzyme.
InterPro; IPR001909; GATase_1.
InterPro; IPR001468; IGPS.
InterPro; IPR001240; PRAI.
InterPro; IPR006221; TrpG_papA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X07071; CAA30107.1; --
EMBL; M14403; AAA32730.1; --
EMBL; M14404; AAA32700.1; --
EMBL; X040643; S06643.
HSSP; Q06129; 1QDL.
                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006221; Tr
Pfam; PF00117; GATase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
207 EQRE 210
                                    ENOO 680
                                                                                                                                         TRPG ASPNG
P05328;
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                                        677
                                                                                                                     TRPG ASPNG
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PIR; B70419; B70419.
Hypothetical protein; Complete proteome.
SEQUENCE 260 AA; 30206 MW; B5D3FB6F37C89BB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E2 GLYCOPROTEIN.
SPIKE PROTEIN S1.
SPIKE PROTEIN S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87085499; PubMed=3025348;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=85159540; PubMed=2984314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gen. Virol. 66:719-726(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M95169; AAA70235.1; -. EMBL; X02342; CAA26201.1; -.
                                                                          Conservative
                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1162
537
1162
                                                                                                                                                127 NGPVMOKKTO
                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=11122;
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19
538
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                                                     Mar
Local Sim-
37;
                                                                                                                                                                                                                                                                  VGL2_IBVB
                                                    Query Match
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                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                     69 KYPE-----DIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS-- 120
                                                                                                                                                                                                                                                                                                                 -----GSLAVT 150
                                                                                                                                                                                                                                                                                                                                                                                    121 GLNFPPNGFVMQKKTQGWEPNTERLFARDGMLIGNNFNALKL.---EGGGHYLCEFKSTYK 177
                                                                                                                                                                                                                                                                                                                                                                                                     151 RYHSLAGTHATIPDCLEVS-----SSVQLADD-----SNKDVİMG---VRHKKLAVE 194
                                                                                                                                                                                                                                                                                        KVYMSGTV-NGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFT 68
                                                                                                                                                                                                                                                                  72; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                      Tryptophan biosynthesis; Isomerase; Lyase; Multifunctional enzyme;
Decarboxylase; Transferase; Glutamine amidotransferase
                                                                                                                                               SYNTHASE
                                                                                                                                              INDOLE-3-GLYCEROL PHOSPHATE SYNTHJ
N- (5'-PHOSPHORIBOSYL)ANTHRANILATE
                                                                                                                                                                                                                                          Score 86; DB 1; Length 770; Pred. No. 5.3;
                                                                                                                                                                                                                                                                   61; Indels
                                                                                                                    Transferase, Glutamine amidotransferase. 219 GLUTAMINE AMIDOTRANSFERASE.
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KTASE (BY SIMILARITY).
KTASE (BY SIMILARITY).
36D8DE5B23097012 CRC64;
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GATASE
GATASE
                                            PRINTS; PRO0006; GATASE.
ProDom; PD001511; IGPS; 1.
TIGRPAMS; TIGR00566; trpG_papA; 1.
PROSITE; PS00442; GATASE TYPE_1; 1.
PROSITE; PS00614; IGPS; 1.
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Pfam; PF00218; IGPS; 1.
Pfam; PF00697; PRAI; 1.
PRINYS; PR00097; ANTSNTHASEII.
PRINYS; PR00099; CPSGATASEI.
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                                                                                                                                                                                                                    82909 MW;
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199
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770 AA;
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16-OCT-2001
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                                                                                                                                                      71 PEDIPDYVKQSFPGRY----TWERIMNFEDGAVCTVSNDSSIQGNCFIXHVKFSGLNFPP 126
                                                                                                                                                                                                                                                                                                            171
                                                                                                                                                                                                                                                                                                                                                      98 ELGIFQSVEEAMGAFLSTALEHGWEEVPKNYVIYHADFVEGGNKLIAAIKTEEGISTYDQ 157
                                                                                                                                                                                                                                  97
                                                                                                                                                                                                46 PENVREFLKENYPEKYKLIENWEELQGEFD------VQKLGGGNEYLVIYRIPEKEFEK
                                                                                                                                                                                                                                                                                                        -GWE--PNTERLFARDGMLIGNNFM-ALKLEGGGHYLCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and sequencing of the gene encoding the spike protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Binns M.M., Boursnell M.E.G., Towley F.M., Brown T.D.K.; "Comparison of the spike precursor sequences of coronavirus IBV arrains M41 and 6/82 with that of IBV Beaudette.", J. Gen. Virol. 67:2825-2831(1986).
-!- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Avian infectious bronchitis virus (strain Beaudette) (IBV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-MaR-2004 (Rel. 13, Last annotation update)
E2 glycoprotein precursor (Spike glycoprotein) (Peplomer protein)
[Contains: Spike protein S1; Spike protein S2].
                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 FKSTYKARKPVKMPGYHYVDRKLDVTNHNKD-YTSVEQREISIARK 216
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                                                                                Indels
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InterPro; IPR002551; Corona S1.
InterPro; IPR002552; Corona S2.
Pfam; PF01600; Corona S1; 1.
Glam; PF01601; Corona S2; 1.
Glycoprotein; Evelope protein; Transmembrane; Signal.
                                                                         71;
6.7%; Score 85; DB 1;
22.3%; Pred. No. 1.8;
tive 28; Mismatches 71
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SEQUENCE FROM N.A.
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RELN_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 PDYVKQSFPGRYTWERIMNFEDGAV---CTVSNDSSIQGNCFIYHVKFSGLNFPPNG--- 128
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P76134; P7755;
P76134; P7755;
P76134; P7755;
P76134; P7755;
P76134; P7755;
P76134; P77755;
P76134; P77755;
P76134; P77755;
P86135; P76161 ydeM.
P8616161                                                                                                                                                                                                                                   (POTENTIAL)
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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       ۷.,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Dayis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                           Alba H., Baba T., Fulta K., Hayashi K., Inada T., Isono K., Alba H., Baba T., Fulta K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori H., Motomura K., Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Yagami H., Takeded J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., "A 570-kb DNA sequence of the Escherichia coli K-12 genome or responding to the 28.0-40.1 min region on the linkage map."; DNA Res. 33:363-377(1996).
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                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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Pfam; PF04055; Radical SAM; I.
Hypothetical protein; Complete proteome.
RSEQUENCE 385 AA; 44518 MW; 964834F73E680329 CRC64;
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Reelin precursor (EC 3.4.21.-) (Reeler protein).
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                                                                                                                                                                                                                                                                                                                        STRAIN=K12;
MEDLINE=97251357; PubMed=9097039;
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Best Local Similarity 19.6%
Matches 55; Conservative
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Rawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Mashio T.,
Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Riingwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Wynshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=95375789; PubWed=7647795;
Hirotsune S., Takahara T., Sasaki N., Hirose K., Yoshiki A.,
Chashi T., Kusakabe W., Muramar Y., Muramatsu M., Watanabe S.,
Nakao K., Katsuki M., Hayashizaki Y.;
"The reeler gene encodes a protein with an EGF-like motif expressed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Reelin is a secreted glycoprotein recognized by the CR-50 monoclonal
                                                                                                                                                                                                          "A protein related to extracellular matrix proteins deleted in the mainse mutant reeler ".
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                           MEDLINE=95231649; PubMed=7715726; D'Arcangelo G., Miao G.G., Chen S.-C., Soares H.D., Morgan J.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                 Royaux I., Lambert de Rouvroit C., D'Arcangelo G., Demirov D., Goffinet A.M.;
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D.Arcangelo G., Farace M.G., Keller F.,
"Reelin is a serine protease of the extracellular matrix.";
J. Biol. Chem. 277:303-309(2002).
                                                                                                                                                                                                                                                                                                                                                                          'Genomic organization of the mouse reelin gene.";
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=98086481; PubMed=9417911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 3044-3461 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 2152-3461 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY.
MEDLINE=97325946; PubMed=9182958;
Schiffmann S.N., Bernier B., Goffinet A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6J; TISSUB=Testis;
MEDLINE-21085660; PubMed=11217851;
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MEDLINE=97141547; PubMed=8987733;
                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurosci. 17:23-31(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pioneer neurons.";
Nat. Genet. 10:77-83(1995).
                                                                                                                                                                                                                                                                                                                                                                                                3enomics 46:240-250(1997).
                                                                                                                                                                                                                               mouse mutant reeler.";
Nature 374:719-723(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001).
musculus (Mouse)
                                                                                                                         IISSUE=Cerebellum;
                                                            NCBI_TaxID=10090;
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Isold=260841-3; Sequence=VSP 005578;

-1 TISSUE SPECIFICITY: The major isoform 1 is neuron-specific. It is abundantly produced during brain ontogenesis by the Cajal-Retzius cells and other pioneer neurons located in the telencephalic marginal zone and by granule cells of the external granular layers of the cerebellum. Expression is located in deeper layers in the developing hippocampus and olfactory bulb, low levels of expression are also detected in the immature striatum. At early developmental stages, expressed also in hypothalamic of ields, tectum and spinal cord. A moderate to low level of expression occurs in the septal area, striatal fields, habenniar nuclei, some thalamic nuclei, particularly the lateral geniculate, the retina and some nuclei of the reticular formation in the central field of the medulla. Very low levels found in liver and kidney. No expression in radial glial cells, cortical plate. Purkinje cells and inferior olivary neurons. The minor isoform 2 is only expressed in non neuronal cells. The minor isoform 3 is found in the same cells as isoform 1, but is almost undetectable in retina and brain stem.

Expression increases up to birth and remains high from post-natal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spinal cond, where it seems to act as a barrier to neuronal migration. Enzymatic activity is important for the modulation of cell adhesion. Binding to the extracellular domains of lipoprotein receptors VLDLR and ApoER2 induces tyrosine phosphorylation of Dabl and modulation of Tau phosphorylation.

-!-SUBGELLULAR LOCATION: Secreted.
-!-ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   day 2 to 11 in both cerebellum and fore/midbrain. Expression declines thereafter and is largely brain specific in the adult.
-!- DOMAIN: The basic C-terminal region is essential for secretion.
-!- PTM: N-glycosylated and to a lesser extent also O-glycosylated.
-!- DISEASE: Defects in reln are the cause of the autosomal recessive reeler (rl) phenotype which is characterized by impaired motor coordination, tremors and ataxia. Neurons in affected mice fail to reach their correct locations in the developing brain, disrupting the organization of the cerebellar and cerebral cortices and other
                                                                                                                                                                                                                                                                                                                                       "Evolutionarily conserved, alternative splicing of reelin during brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hiesberger T., Trommsdorff M., Howell B.W., Goffinet A.M., Mumby M.C., Cooper J.A., Herz J.,

"Direct binding of Reelin to VLDL receptor and ApoE receptor 2 induces tyrosine phosphorylation of disabled-1 and modulates tau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20359755; PubMed=10880573;
Yip J.W., Yip Y.P.L., Nakajima K., Capriotti C.;
"Reelin controls position of autonomic neurons in the spinal cord.";
Proc. Natl. Acad. Sci. U.3.A. 97:8612-8616(2000).
-!- FUNCTION: Extracellular matrix serine protease that plays a role in layering of neurons in the cerebral cortex and cerebalum. Regulates microtubule function in neurons and neuronal migration.

Affects migration of sympathetic preganglionic neurons in the
                                                                                                                                                                                                                                    Lambert de Rouvroit C., Bernier B., Royaux I., de Bergeyck V.,
"Reelin mRNA expression during mouse brain development."; Eur. J. Neurosci. 9:1055-1071(1997).
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                                                                                                                                          SPLICING, AND TISSUE SPECIFICITY
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                                                                                                                                                                                            MEDLINE=99263436; PubMed=10328932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20036019; Pubmed=10571241;
                                                                                                                                                                                                                                                                                                                                                                                         development.";
Exp. Neurol. 156:229-238(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING TO VLDLR AND APOER2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphorylation.";
Neuron 24:481-489(1999).
                                                                                                                                                                                                                                                                                          Goffinet A.M.;
                                                                                                                                          ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=1;
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                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2080 YYAGTTQGWRREVVHFGKLHLCG-----SVRFRWYQGFYPAGSQPVTWAIDNVYIGPQ 2132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2193 RKCGILSSGNNLFFNEDGLRMLVTRDLDLS-----HARFVQFFMRLGCGKGVPDFRSQP 2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2247 VLLQYSINGGLSWSLLQEFLFSNSSNVGRYIALEMPLKARSGSTRLRWWQPSENGHFYSP 2306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SGINFPPNGP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YMSGTVNGHYFEVEGDGK----GKPYEGEQTVRLAVTKG----GPLPFAWDI----LSPQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SIPFTKYPEDIPDYVKQSFPGRYTWERIMNF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                         Hydrolase, Serine protease, Developmental protein, Matrix protein, Cell adheaion, EGF-like domain, Glycoprotein, Repeat, Signal, Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 3461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2307 WVIDOILIGGNI ----SGNTVLEDDFSTLDSRKWLLHPG 2341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARKPVKMPG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75;
                                                                                                                          EMBL; U24703; AA591599.1; -.
EMBL; D63520; BAA09788.1; -.
EMBL; AK017094; BAB30592.1; -.
MGD; MGI:103022; Reln.
GO; GO:0007420; Peln.
GO; GO:0007420; Peln.
GO; GO:0007427; P:cell migration; IMP.
InterPro; IPR005209; EGF like.
InterPro; IPR005209; EGF like.
InterPro; IPR002801; Reeler.
Pfam; PF02012; BNR; 15.
Pfam; PF02012; BNR; 15.
Pfam; PF02014; Reeler.
Pfam; PF02014; Reeler.
Pfam; PF02014; Reeler; 1.
SMART; SM00181; EGF; 3.
PROSITE; PS01186; EGF 2; 6.
PROSITE; PS01186; EGF 2; 6.
PROSITE; PS01186; EGF 2; 5.
         -!- SIMILARITY: Belongs to the reelin family.
-!- SIMILARITY: Contains 8 EGF-like domains.
-!- SIMILARITY: Contains 15 BNR repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.3%; Pred. .v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 83.5; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                      EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 7.
EGF-LIKE 7.
EGF-LIKE 7.
EGF-LIKE 7.
EGF-LIKE 8.
                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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1796
2161
2509
2884
3260
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  laminated regions.
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11409
11765
2129
2478
2853
3228
593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---FAWEFLTSDKWMGMEPDKLYVTIH 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 PEDMEAY -----FWDIGEBSRII-----RIEGN ----FWDIGEGPSG-- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP + diphosphare + L-alanyl-ERNA(Ala).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00980; TRNAŠYNTHALA.
TIGRRAMS; TIGR00344 alas; 1.
PROSITE; PS50860; AA TRNA LIGASE II ALA; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                    10-OCT-2003 (Rel. 42, Created)
110-OCT-2003 (Rel. 42, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS).
ALAS OR SAV1618 OR SA1446.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-MISO, ATCC 700699, and N315;
RUTAIN-MISO, ATCC 700699, and N315;
RUTODA M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RUTODA M., Ohta T., Yohiyama I., Baba T., Tian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba 'Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79;
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                                                                                                                                                                                                                                                 Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
SEQUENCE 876 AA; 98538 MW; 2B2BC79041AC264F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PNTEIFYDR-GEAYGODDPAEEMYPGGEN--
876 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 DRKLDV-----TNHNKD--YTSVEQREI 211
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21.9%; Pred. No. 13;
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InterPro; IPR003156; DHHA1.
InterPro; IPR003138; tRNA-synt_2c.
InterPro; IPR006193; tRNA_synt_Ala.
Pfam; PF02272; DHHA1; 1.
Pfam; PF01411; tRNA-synt_2c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP003362; BAB57780.1; -. EMBL; AP003134; BAB42710.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=158878, 158879;
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   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 TARHHIFFEMLGNFSIGDYFKQEAIE------FAWEFLISDKWMGMEPDKLYVTIH 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 PEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPV 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 PEDMEAY-----NIWHKDIGLESRII------RIEGN------FWDIGEGPSG-- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 MOKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARKPVKMPGYHYV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVNGH-YFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIP----FTKY 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diphosphate + L-alanyl-tRNA(Ala).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-11 aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS).
                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; Rubmed=12044378;
MEDLINE=22040717; Rubmed M., Yuzawa H., Aoki K.-I., Oguchi A., Nabar Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K., "Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      876 AA; 98505 MW; 5D9D662D8DDAEDFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PNTEIFYDR-GEAYGODDPAEEMYPGGEN---
                                                                                                                                                           Staphylococcus aureus (strain MW2).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERYLEVWNLVFSEFNHNKDHSYTPLPNKNI 225
876 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.5%; Score 82.5; D
Best Local Similarity 21.9%; Pred. No. 13;
Matches 46; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF 00036; -; 1.
InterPro; IPR003156; DHHA1.
InterPro; IPR002318; tRNA-synt_2c.
InterPro; IPR006193; tRNA_synt_Ala.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP004827; BAB95433.1; -.
                                                                                                                                                                                                                                                                                              359:1819-1827 (2002)
                                                                         STANDARD;
                                                                                                                                                                                 NCBI_TaxID=196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
SEQUENCE 876 AA
                                                                                                                                                                                                                                                                                    acquired MRSA.";
                                                                                                                                                 ALAS OR MW1568.
                                                                       SYA STAAW
Q8NW87;
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MEDIAINS 10 PubMed=11859360;

WEDGAINS 21948401; PubMed=11859360;

Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Bodouros V., Feat N., Hayles J., Basham D., Bowaman S., Brown D., Brown B., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin M., Davis P., Feltwell T., Fraser A., Gonlins M., Connor R., Davis P., Feltwell T., Fraser A., A danes K., Jones L., Jones M., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J., McDonald S., Saudares R., Saudares R., Saudares R., Saudares R., Stevens K., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Anylor K., Taylor K., Taylor K., Walsh S.V., Warren T., Whitchead S., McDoward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels B., Rieger M., Schaefer M., McHler-Auer S., Berrym K., Langer I., Berger M., Schaefer M., McHler S., Barger P., Zimmermann W., Wedler H., Manbutt R., Purnelle B., Goffeu A., Calleu E., Dreano S., Gloux S., Lelaure V., Mottier S., Goffeu A., Caucado L., Jimenez J., Sanchez M., Garzon A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Abhakovski G.V., Ussery D., Barrell B.G., Nurse P., Marker M., Reinher G., Schizosaccharomyces pombe.";

My Harder M. Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., Marker B., M
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SEQUENCE 248 AA; 28003 MW; A23EF9D59E597E43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                            Hypothetical protein C13C5.04 in chromosome I
                                                                                     (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast)
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STANDARD:
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164 VDVPEGFELLGSTEDCEFQIFYKPRQALTFQGHPEFSTEVVNTMVKVLRGTEVFTE-QQK 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          development.";

Exp. Neurol. 156:229-238 (1999)

-:- FUNCTION: Extracellular matrix serine protease that plays a role in layering of neurons in the cerebral cortex and cerebellum. Regulates microtubule function in neurons and neuronal migration. Affects migration of sympathetic preganglionic neurons in the spinal cord, where it seems to act as a barrier to neuronal migration. Enzymatic activity is important for the modulation of cell adhesion. Binding to the extracellular domains of lipoprotein receptors VLDLR and ApoER2 induces tyrosine phosphorylation of Dab1 and modulation of Tau phosphorylation (By similarity).

-:- SUBUNIT: Binds to the ectodomains of VLDLR and ApoER2 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
DISBASE: Defects in Reln are the cause of creeping, which is characterized by tremor, gait ataxia, cerebellar hypoplasia and abnormal neuronal migration (particularly in the cerebral cortex and hippocampus). The mutation is due to a nucleotide insertion at codon 1892 which results in a translational frameshift and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isoid=PS8751-3; Sequence=VSP_005580; TISSUE SPECIFICITY: Abundantly produced during brain ontogenesis by the Cajal-Retzius cells and other pioneer neurons located in the telencephalic marginal zone and by granule cells of the external granular layer of the cerebellum.

DOMAIN: The basic C-terminal region is essential for secretion (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Evolutionarily conserved, alternative splicing of reelin during brain
                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                      Yokol N., Namae M., Wang H.-W., Kojima K., Fuse M., Yasuda K., Serikawa T., Seino S., Komeda K.; "Rat neurological disease creeping is caused by a mutation in the reelin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99263436; PubMed=10328932;
Lambert de Rouvroit C., Bernier B., Royaux I., de Bergeyck V.,
Goffinet A.M.;
                                                                                                                                                                                                                                                                                 Kikkawa S., Terashima T.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
SUBCELLULAR LOCATION: Secreted (By similarity)
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=3;
                                                                                                                      P58751; Q80T65;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
P0-CCT-2003 (Rel. 42, Last annotation update)
Reelin precursor (EC 3.4.21.-).
                                                                                                             PRT; 3462 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P58751-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                           3rain Res. Mol. Brain Res. 112:1-7(2003).
                                                                                                                                                                                                                                                                                                                                              MEDLINE=22557166; PubMed=12670697;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND DISEASE.
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                              STANDARD;
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                        EISIAR 215
                                                EEALKR 228
                                                                                                                                                                                                                                                                                                                                   TISSUE=Cerebellum;
                                                                                                                                                                                                                                   NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                      Hydrolase; Serine professe; Developmental protein; Matrix protein; Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal; Alternative splicing.

SIGNAL POTENTIAL.
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        SIMILARITY: Belongs to the reelin family. SIMILARITY: Contains 8 EGF-like domains. SIMILARITY: Contains 15 BNR repeats.
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EMBL; AB062680; BAC75467.1; -.
InterPro; IPR002860; GF BIR.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
truncation of the protein.
                                                                                                                                                                                                                             Pfam; PF02012; BNR; 15.
Pfam; PF00008; EGF; 3.
Pfam; PF02014; Reeler; 1.
SMART; SM00181; EGF; 6.
PROSITE; PS00022; EGF 17.
PROSITE; PS01186; EGF 2; 6.
PROSITE; PS01186; EGF 2; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |::| | ::| ::| ::| | ::| | ::| | ::| | ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
                                                                                                                                                                                                                                                                                                                                                                                                                                          2081 YYAĞITQĞWRREVVHFGKLHLCĞ-----SVRFRWYQĞFYPAĞSQÞVTWALDNVYIGÞQ 2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2194 RKCGILSSGNNLFFNEDGLRMLVTRDLDLS-----HARFVQFFMRLGCGKGVPDPRSQP 2247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2248 VLLQYSLNGGLSWSLLQEFLFSNSSNVGRYIALEMPLKARSGSTRLRWWOPSENGHFYSP 2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --EDGAVCTVSNDSSIQGNCFIYHVKF-----SGLNFPPNGP 129
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-!- FUNCTION: Involved in the mineralization and structural organization of enamel. Involved in the extension of enamel during the secretory stage of dental enamel formation.

-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.

-!- TISSUE SPECIFFCITY: Expressed in tooth particularly in odontoblast, ameloblast and cementoblast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 CQ----YGSI-----PFTKYPEDIPDYVKQSFPGRYTWERIMNF----
                                                                                                                                                                                                                                                                                                                                                                                         12 YMSGTVNGHYFEVEGDGK----GKPYEGEQTVRLAVTKG----GPLPFAWDI----LSPQ
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                        75; Indels 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hu C.-C., Qian Q., Zhang C., Fukae M., Uchida T., Simmer J.P., "cDNA sequence of human enamelin."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                     ; Score 81.5; DB 1; Length 3462;
; Pred. No. 80;
25; Mismatches 75; Indels 125;
                                                                                                                                                                                                                                 FCCF89B090E035F6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 -ARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARKPVKMPG 186
(GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .)
                     N-LINKED (GLCNAC. .)
N-LINKED (GLCNAC. .)
Missing (in isoform 2).
/FTIG=VSP_005579.
                                                                                                                       Missing (in isoform 3)
                                                                                                                                                                           -> R (IN REF. 2)
-> L (IN REF. 2)
                                                                                                                                                     005580.
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16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1142 AA
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H -> R (IN
V -> L (TN
N-LINKED
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2714 2714 V ->
3462 AA; 387525 MW;
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Similarity 19.9%;
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CARBOHYD
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases.
Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This magnesium-dependent enzyme catalyzes the hydrolysis of ATP coupled with the translocation of calcium from the cytosol of ATP coupled with the translocation of calcium to the sarcoplasmic reticulum lumen. Contributes to calcium to the sarcoplasmic reticulum lumen. Contributes to calcium to the sarcoplasmic reticulum lumen. Contributes to calcium By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 NGHYFEVEGDGKGKPYEGEQTVRLAVTKG-----GPLPFAWDILSPQCQYGSIPFTKYPE
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CATALYTIC ACTIVITY: ATP + H(2)O + Ca(2+)(Cis) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1990 (Rel. 13, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 42, Last annotation update)
Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 (EC 3.6.3.8)
(Calcium pump 1) (SRRCA1) (SR Ca(2+)-ATPase 1) (Calcium-transporting ATPase sarcoplasmic reticulum type, fast twitch skeletal muscle isoform) (Endoplasmic reticulum class 1/2 Ca(2+) ATPase).
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Karin N.J., Kaprielian Z., Fambrough D.M.;
"Expression of avian Ca2+-ATPase in cultured mouse myogenic cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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                                                                                                                                                                                                               GO; GO:0005578; C:extracellular matrix; NAS.
GO; GO:0030345; F:structural constituent of tooth enamel; NAS.
GO; GO:0030282; P:bone mineralization; NAS.
GO; GO:0042476; P:odontogenesis; NAS.
Blomineralization; Extracellular matrix; Glycoprotein; Signal. SIGNAL.

1 39 POTENTIAL.
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                                or send an email to license@isb-sib.ch).
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                                                                                        EMBL; AF125373; AAG43242.1; -. EMBL; AF210247; AAF73847.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 DIPDYVKQSFP-GRYTWE 89
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                                                                                                                                                       Genew; HGNC:3344; ENAM.
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                                                             (By Similarity).

SUBCELLULAR LOCATION: Integral membrane protein. Sarcoplasmic and endoplasmic reticulum.

SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IIA.
            low calcium concentrations. Dephosphorylated PLN decreases the apparent affinity of the Arpsase for calcium. This inhibition is regulated by the phosphorylation of PLN (By similarity). SUBUNIT: Associated with sarcolipin (SLN) and phospholamban (PLN)
ENZYME REGULATION: Reversibly inhibited by phospholamban (PLN) at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY
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CYTOPLASMIC (BY SIMILARITY).
INTERACTS WITH PHOSPHOLAMBAN 1 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Calcium transport; Transmembrane; Phosphorylation;
Magnesium; ATP-binding; Metal-binding; Calcium-binding;
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MAGNESIUM (BY SIMILARITY).
CALCIUM 2 (VIA CARBONYL OXYGEN)
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ACACIUM 2 (VIA CARBONYL OXYGEN)
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3 (BY SIMILARITY).
LUMENAL (BY SIMILARITY).
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CYTOPLASMIC (BY SIMILARITY)
5 (BY SIMILARITY).
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6 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
7 (BY SIMILARITY).
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LUMENAL (BY SIMILARITY).
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LUMENAL (BY SIMIL
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INTERPOS IPRO05782; Calcium ATPASE.
INTERPOS IPRO06782; Calcium ATPASE.
INTERPOS IPRO06089; Cation ATPASE C.
INTERPOS IPRO080250; B1-E2 ATPASE C.
INTERPOS IPRO08035; H ATPASE.
INTERPOS IPRO06934; Hydrolase.
Pfam; PF00609; Cation ATPASE.
Pfam; PF00609; Cation ATPASE.
Pfam; PF00702; Hydrolase; I.
PRINTS; PR00119; CATATPASE.
IGREPMS; TIGRO1119; CATATPASE.
TIGREPMS; TIGRO1116; ATPASE-IIAL Ca; I.
TIGREPMS; TIGRO1116; ATPASE-IIAL Ca; I.
TIGREPMS; TIGRO1116; ATPASE-IIAL Ca; I.
TIGREPMS; TIGRO1116; ATPASE-IIAL Ca; I.
TIGREPMS; TIGRO1116; ATPASE-IIAL Ca; I.
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                                                                                                                                                                                                                                                                                                                                      147 ARDG-----MLIGNNFMALKLEGGGHYLCEFKSTYKARKPVKMPGYHYVDRKLDVTNHNK 201
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MEDLINE=98409534; PubMed=9736608;
Meurer J., Pluecken H., Kowallik K.V., Westhoff P.;
Meurer J. pluecken H., Kowallik K.V., Westhoff P.;
A nuclear-encoded protein of prokaryotic origin is essential for the stability of photosystem II in Arabidopsis thaliana.";
EMBO J. 17:5286-5297(1998).
                                                                                                                                                                                                                                           515 KGAP----EGVIDRCNYVRVGTTRVPLTPAVKEKILAVIKEWGTGRDTLRCL----A
                                                                                                                                                                                                                  45 KGGPLPFAWDILSPQCQYGSIPFTKYP----EDIPDYVKQSFPGRYTWERIMNFEDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Columbia;
MEDLINE=22954850; PubMed=14593172;
Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor.
HCF136 OR AT5Q23120 OR MYJ24.11.
Arabidopsis thaliana (Mouse-ear cress).
Enbaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structural analysis of Arabidopsis thaliana chromosome 5. II. Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned PI clones.";
DNA Res. 4:291-300(1997).
                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                       63;
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15-JUL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Photosystem II stability/assembly factor HCF136, chloroplast
                                                                                                                                                             DB 1; Length 994;
                                                                                                                                                                                        73; Indels
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                                                    SIMILARITY).
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24; Mismatches
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MEDLINE=20181125; PubMed=10718197;
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994 AA;
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SEQUENCE FROM N.A.
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Matches 50; <
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                                                                                                                                                                      Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y., Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P., Chao G., Choy N., Enju A., Goldmath A.D., Gurial M., Hansen N.F., Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M., Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J., Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y., Vuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOTOSYSTEM II STABILITY/ASSEMBLY FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGREAMS; TIGRO1409; TAT signal seq; 1.
Chloroplast; Thylakoid; Transit peptide; Photosystem II; Membrane.
IRANSIT 1 53 CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.2%; Score 79; DB 1; Length 403; 23.9%; Pred. No. 10;
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EMBL; AB006708; BAB09829.1; -.
EMBL; AY045691; AR74049.1; -.
PIR; T51828; T51828.
IntexPro; IPR002860; GH BNR.
IntexPro; IPR0053811; Tat.
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79
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11;

42; Gaps

25; Mismatches 89; Indels

49; Conservative

Best Local Similarity Matches 49; Conserv

Search completed: August 12, 2004, 06:20:08 Job time : 16.2008 secs

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August 12, 2004, 06:12:47; Search time 60.1168 Seconds (without alignments) 1212.385 Million cell updates/sec
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1268
1 SVIAKQMTYKVYMSGTVNGH.....SIARKPLVACCFFRVKSRHK 231
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                            1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_rodent:*
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sp_unclassified:*
sp_rvirus:*
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sp_archeap:*
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: sp_archea:*
: sp_bacteria:*
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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                                                                  OM protein
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Q95p04 goniopora t Q9u6y8 discosoma s Q9gtj7 discosoma s Q9u6y7 discosoma s Q8t6u0 dendronepht Q963f5 montastraea Q720w4 montastraea montastraea clavularia montastraea montastraea montastraea montastraea montastraea montastraea montastraea Description 0720w5 09u6y3 0720w6 0720w9 0962p9 0720w8 095ua7 SUMMARIES 095504 0906YB 0906YJ 0906YJ 0963E5 0963E5 0720W5 0720W6 0720W6 0962P9 0962P9 0962P9 Query Match Length DB 672 667.5 665.5 665.5 665.5 665.5 665.5 664.5 1138 780 750 737.5 704.5 703 Score Result No. 

Q720W7 montastraea Q8mu48 montastraea Q95vt0 montastraea O81618 trachvohv11		Q8t5e8 ricordea fl Q8isf8 parasicyoni Q8mmal aqaricia aq Q8mu46 ricordea fl	condylact radianthu anemonia condylact	condylact radianthu meandrina scolymia	Q86, ve meandrina m Q816t9 radianthus Q906y6 anemonia ma Q815e7 condylactis Q906y5 zoanthus sp Q9bly9 renilla mue
5 Q7Z0W7 5 Q8MU48 5 Q95VT0 5 O816.18				5 Q8MU45 5 Q86LV4 5 Q86LV7 5 Q8T5F0 5 Q8T5F3	5 Q86LV8 5 Q8T6T9 5 Q9U6Y6 5 Q9U6Y5 5 Q9BLY9
234 224 227	231 231 231 231	231 231 239	2227 2227 2228	232 223 214 235 235	214 225 229 231 238
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654.5 652 651.5		586.5 584.5 578	566.5 562.5 562.5 561	20 00 111 111 00 02	530 529.5 529.5 519.5 485.5 482.5
118	0 12 12 12 12 12 12 12 12 12 12 12 12 12	25 27 28 28		2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 4 4 4 4 0 11 2 2 4 4 4 5

#### ALIGNMENTS

		0	61	120
04 095P04 PRELIMINARY; PRT; 221 AA. 095D04, 025D04, 025C-2010 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2003 (TrEMBLrel. 25, Last annotation update) GPP-like chromoprotein. Goniopora tenuidens. Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia; Fungina; Poritidae; Goniopora. NCBI TaxID=75301;	SEQUENCE FROM N.A. MEDILINE=21538656; PubMed=11682051; Gurskaya N.G., Fradkov A.F., Terskikh A., Matz M.V., Labas Y.A., Gurskaya N.G., Fradkov A.F., Terskikh A., Matz M.V., Labas Y.A., Martynov V.I., Yanushevich Y.G., Lukyanov K.A., Lukyanov S.A.; "GPP-like chromoproteins as a source of far-red fluorescent proteins(1)."; 16-20(2010).  EMBL, AF383156; AAL37542.1; - GO; GO: 0006091; P:energy pathways; IEA.  InterPro; IPR000786; Green_fl_protein.  Probom, P0013756; Green_fl_protein.  Probom, P0013756; Green_fl_protein; 1.  Probom, P0013756; Green_fl_protein; 221 AA; 24918 WW; 93F9F4B5C2003C84 CRC64;	Query Match 89.7%; Score 1138; DB 5; Length 221; Best Local Similarity 95.0%; Pred. No. 5e-100; Matches 209; Conservative 5; Mismatches 6; Indels 0; Gaps	1 SVIAKOMTYKVYMSGTVNGHYPEVBGDGKGKPYEGEQTVRLAVTKGGPLPPAWDILSPQC 60	61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 12
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36; Mismatches
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MEDLINE=99436614; PubMed=10504696;
                            Discosoma sp. SSAL-2000.
Eukaryota, Metazoa, Cnidar
Discosomatidae, Discosoma.
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Red fluorescent protein.
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                                                                         NCBI_TaxID=137428;
                                                                                                     SEQUENCE FROM N.A.
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                         121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
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                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia;
Discosomatidae; Discosoma.
NCBI_TaxID=86600;
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SEQUENCE FROM N.A.

MAZZ M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G.,
Markelov M.L., Lukyanov S.A.;

Markelov M.L., Lukyanov S.A.;

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF168419; AAF03369.1; --
PDB; 1G7K; 07-NOV-01.

PDB; 1GGX; 06-DEC-00.

PDB; 1GGX; 06-DEC-00.
                                                                                                                                                                                                                                                                                                                                                                    Matz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G., Markelov M.L., Lukyanov S.A.; "Fluorescent proteins from nonioluminescent Anthozoa species."; Nat. Biotechnol. 17:969-973(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRVKSRH 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 61.5%; Score 780; DB 5; Length 225; Best Local Similarity 62.6%; Pred. No. 5.3e-66; Matches 144; Conservative 28; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIGURE FEGURES, CIF, A. T. PERUNITS, PROJESS, GREEN I protein; 1.

PRODOM; PD013756; Green II protein; 1.

SEQUENCE 225 AA; 25931 MW; FBF9A5369778F689 CRC64;
                                                                   PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVA 220
                                                                                       PVKMPGYHYVDRKLDVTNHNIDYTSVEQCEISIARKPVVA 221
                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Last sequence update)
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InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
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(TrEMBLrel. 16, I
(TrEMBLrel. 25, I
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                                                                                                                                                                                                                                                  Fluorescent protein FP583,
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01-MAR-2001
01-OCT-2003
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RESULT 3 Q9GTJ7

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RESULT 2
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61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
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Cnidaria, Anthozoa; Zoantharia, Corallimorpharia;
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Discosomatidae; Discosoma.
NCBI_TaxID=105400;
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EMBL; AF168420; AAF03370.1; -.. GO, GO:0006091; P:energy pathways; IEA.

InterPro; IPR009017; GFP_like.

InterPro; IPR000786; Green_fl_protein.

Pfam; PF01353; GFP; 1.
                                                                                                                                                                                                             Lukyanov S.A.;
"Novel fluorescent protein from Discosoma coral and its mutants possesses a unique far-red fluorescence.";
FEBS Lett. 479:127-130(2000).
EMBL; AF21221; 1BFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 230;
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                                                                                                                                                                                 Fradkov A.F., Chen Y., Ding L., Barsova E.V., Matz M.V.,
                                                                                                                                                                                                                                                                                                                                                                                   GO, GO:0006091, P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP100RESCENT.
PRINTS; PR01329; GFP100RESCENT.
ProDom; PD013756; Green_fl_protein; 1.
SRQUENCE 230 AA; 26370 MW; 5215B1B436D67E51 CRC64;
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 232 AA; 26435 WW; AA8F18EEE283CE4D CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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121 GINFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kelmanson I.V., Marz M.V.;
"Molecular Basis and Evolutionary Origins of Color Diversity in Great
Star Coral Montastraea cavernosa (Scleractinia: Faviida).";
Mol. Biol. Evol. 20:1125-1133 (2003).
EMBL; AY181557; AA061603.1; -.
SEQUENCE 225 AA; 25827 MW; A600ADD716C5921E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Montastraea cavernosa (great star coral).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
Faviina; Faviidae; Montastraea.
                                                                      Montastraea cavernosa (great star coral).
Eukaryota, Metazoa, Chidaria, Anthozoa; Zoantharia; Scleractinia;
Faviina; Faviidae; Montastraea.
NCBI_TaxID=63558;
                                                                                                                                               SEQUENCE FROM N.A.
Lesser M.P., Barry T.M., Mazel C., Matz M.V., Lukyanov S.A.,
Lesser M.P., Gorbunov M., Kolber Z.;
"Green fluorescent proteins in Caribbean Scleractinian corals.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF184689; AAK62982.;
GO, GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR0090186; Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                       Length 225;
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PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 225 AA; 25847 MW; 77DE7D7C616929AF CRC64;
              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 55.8%; Pred. No. 3.3e-58;
Matches 120; Conservative 43; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                     55.4%; Score 703; DB 5; 56.3%; Pred. No. 1.1e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 PVKMPGYHYVDRKLDVTNHNKDYTSVEOREISIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 AA
                                                                                                                                                                                                                                                                                                                                                                                                    46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=mc6;
MEDLINE=22689801; PubMed=12777529;
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 56.3%
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=63558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7Z0W4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
                                                                                                                                                                                                    QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
                                                                                                                                                    66 QYGNKAFVHHPDNIHDYLKLSFPEGYTWERSMHFEDGGLCCITNDISLTGNCFYYDIKFT 125
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                                                                              6 SVIKEEMLIDLHLEGTFNGHYFEIKGKGKOOPNEGTNTVTLEVTKGGPLPFGWHILCPQF
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                                                              SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
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                                 Gaps
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Eukaryota, Metazoa, Cnidaria, Anthozoa, Alcyonaria, Alcyonacea,
Nephtheidae, Dendronephthya.
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   Length 232;
Score 737.5; DB 5; Length Pred. No. 6e-62; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 236 AA; 26840 WW; CE1707CFF9334A90 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                 181 -PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIAR 215
                                                                                                                                                                                                                                                                 186 AALKWPGYHYVDTKLVIWNNDKEFWKVEEHEIAVAR 221
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                               Matches 129; Conservative
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Best Local Similarity
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                                                                                                          QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Cyan fluorescent protein.
Montastraea cavernosa (great star coral).
Mostastraea Cavernosa, Chidaria, Anthozoa, Zoantharia, Scleractinia, Faviidae; Montastraea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kelmanson I.V., Matz M.V.;
"Molecular Basis and Evolutionary Origins of Color Diversit
Star Coral Montastraea cavernosa (Scleractinia: Faviida).",
Mol. Biol. Evol. 20:1125-1133(2003).
EMBL; AY181556; AA061602.1; -
SEQUENCE 225 AA; 25843 MW; 13708587B7D93E35 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 53.4%
Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 VIKPDMKIKIKNAGGNVNGHAFVIEGEGEGKPYDGTHTINLEVKEGAPLPFSYDILSNAFQ 104
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"Molecular Basis and Evolutionary Origins of Color Diversity in Great Star Coral Montastraea cavernosa (Scleractinia: Faviida).";
Mol. Biol. Evol. 20:1125-1133 (2003).
EMBL; AXI81555; AA0616611.1. -.
SEQUENCE 227 AA; 26055 MW; 4BE2CB64FDB0E890 CRC64;
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MEDLINE=99436614; PubMed=10504696;
Matz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G.,
Markelov M.L., Lukyanov S.A.;
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Eukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Scleractinia,
Faviina, Faviidae, Montastraea.
                                                                                             "Fluorescent proteins from nonbioluminescent Anthozoa species.";
Nat. Biotechnol. 17:966-973 (1999).
BMBL; AFI68424; AAF03374.1; -.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR000017; GFP like.
InterPro; IPR000786; Green_fl_protein.
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PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 266 AA; 30450 MW; B4E97406E2708854 CRC64;
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VKLPDYHFVDHRIEILNHDKDYNKVTLYENAVARYSLL 262
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 52.8%; Score 670; DB 5; Local Similarity 54.6%; Pred. No. 1.8e-55; les 119; Conservative 39; Mismatches 60.
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MEDLINE=22689801; PubMed=12777529;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Green fluorescent protein.
Green fluorescent grotein.
Eukaryota; Metazoa; Gnidaria; Anthozoa; Zoantharia; Scleractinia; Favilna; Favilna; Montastraea.
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"Molecular Basis and Evolutionary Origins of Color Diversity in Garacterial Basis and Evolutionary Origins of Color Diversity in Star Coral Montestraea cavernosa (Scleractinia: Faviida).";
Mbl. Biol. Biol. Evol. 20:1125-1133 (2003).
EMBL, AY181553; AA061599-11,
SEQUENCE 227 AA; 26017 MW; 5E312C54EA47F589 CRC64;
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                                                                             Length
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Pfam; PF01353; GFP; 1.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 227 AA; 26017 MW; 5E312C54EA47F589 CRC64;
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                                                                                                                  58;
                                                                               DB 5;
                                                                           Query Match 52.5%; Score 665.5; DB Best Local Similarity 53.4%; Pred. No. 4e-55; Matches 118; Conservative 42; Mismatches
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Q95UA7;
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Q7ZOW8
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"Molecular Basis and Evolutionary Origins of Color Diversity in Great
"Molecular Basis and Evolutionary Origins of Color Diversity in Great
Star Coral Montastraea cavernosa (Scleractinia: Faviida).";

Mol. Biol. Evol. 20:1125-1132-20:113-133 (2003).

EMBL; AY181552; AA061598.1; -.

SEQUENCE 225 AA; 25822 MW; 830871F6936953E2 CRC64;
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Faviina, Faviidae, Montastraea.
NCBI_TaxID=48498;
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Eukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Scleractinia,
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                                                                  178 ARKPVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPL 218
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                                                                                                                                                                                                                    (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                              Faviina; Faviidae; Montastraea.
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Matches 118; Conservative
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MEDLINE-21927629; PubMed=11929996;
A Labas Y.A., Gurskaya N.G., Xanushevich Y.G., Fradkov A.F.,
Lukyanov K.A., Lukyanov S.A., Matz M.V.;
Lukyanov K.A., Lukyanov S.A., Matz M.V.;
Tukyanov K.A., Lukyanov S.A., Matz M.V.;
Torical Avil, Acad. Sci. U.S.A. 99:4256-4261(2002).
Rede, Avil, Aak71335.1;
Rembl, Avil, Acad. Sci. U.S.A. 99:4256-4261(2002).
Rembl, Avil, Acad. Sci. U.S.A. 99:4256-4261(2002).
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 15, Last annotation update)
Cyan fluorescent protein (Fragment).
Gyan fluorescent protein (Fragment).
Eukaryota, Metazoa; Gnidaria; Anthozoa; Zoantharia; Scleractinia; Faviina; Faviidae; Montastraea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Montasfraea cavernosa (great star coral).
Eukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Scleractinia,
Favilna, Favildae, Montastraea.
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                                                                                                                                                                                                                                                                   Falkowski P.G., Sun Y.;

Falkowski P.G., Sun Y.;

Falkowski P.G., Sun Y.;

"Montastraea cavernosa fluorescent protein.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AYOS6460; AAL17905.1;

GO; GO:0006091; P:energy pathways; IEA.

InterPro; IPR009017; GFP_like.

InterPro; IPR00786; Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 AA; 25775 MW; 52DE2F716D083524 CRC64;
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PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 53.49
Matches 117; Conservative
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DB 5; Length 234;

51.7%; Score 655.5;

Query Match

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62 YGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQ----GNCFIYHVK 118
                                                                                                                  119 FSGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKA 178
                                            61
                                                         10 VIKPDMKWKLRMEGAVNGHKFVVEGDGKGKPFDGTQTMDLTVIEGAPLFFAYDILTTVFD
                                         2 VIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQ
               Gaps
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                 Indels
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 Pred. No. 3.7e-54;
 al Similarity 54.1%; Pred. No. 3.7e-119; Conservative 38; Mismatches
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Sequence 7, Appli
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Sequence 20, Appli
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Sequence 67, Appli
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Sequence 12, Appli
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                                                                                                                                                                                                                                                                1 SVIAKQMTYKVYMSGTVNGH......SIARKPLVACCFFRVKSRHK 231
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| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US07_MEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 US-10-315-920-6

1 US-10-315-920-4

1 US-10-315-920-4

5 US-10-314-936-2

5 US-10-314-936-4

5 US-09-999-745-67

US-09-999-745-67

US-09-965-538-12

US-09-865-538-12

US-09-865-538-12

US-09-865-291-12

US-10-132-067-4

2 US-10-132-067-4

3 US-10-121-258-1
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                                                                                                                                                                                                                                                                                                                                                                           1292805 seqs, 313927144 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                      - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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equence 2, equence 56 equence 32	equence 13, equence 2, equence 2, equence 1,	33, 76	equence 10 equence 6, equence 24 equence 44	40 12 12 12 15 16 16	Sequence 8, Appli Sequence 16, Appl Sequence 16, Appl Sequence 46, Appl Sequence 6, Appl Sequence 6, Appli Sequence 4, Appli
10-315-920- 10-370-570- 10-406-618-		-214-932- -343-977- -214-932- -423-688A	10-006-922-1 10-121-258-6 10-121-258-2 10-006-922-4 10-081-864-1	10-121-258 10-724-178 10-006-922 10-161-403 10-133-973 10-370-570	10-724-178- -10-121-258- -10-724-178- -10-370-570- -10-133-922- -10-133-922-
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16 17 18	19 20 21 22 22	2 4 2 2 2 2 2 4 2 4 2 5 6 5 6	228 330 321	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

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Sequence 7, Application US/10442148A

Sequence 7, Application US/20040014242A1

Publical INFORMATION:
GENERAL INFORMATION:
APPLICANT: IMAKURA, MASAHIRO
APPLICANT: INFORMATION:
APPLICANT: INFORMATION:
PROCESS FOR IMMOBILIZING ORIENTATION-CONTROLLED PROTEIN AND TITLE OF INVENTION: PROCESS FOR IMMOBILIZING PROTEIN USING THE SAME FILE REFERENCE: 04583.0103-00000

CURRENT APPLICATION NUMBER: US/10/442,148A

CURRENT FILING DATE: 2003-05-21

PRIOR APPLICATION NUMBER: JP 2002-148950

PRIOR FILING DATE: 2002-05-23

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.2

SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 QYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVATVTQDSSLQDGCFIXKVKFI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.9%; Score 785; DB 15;
62.6%; Pred. No. 1.3e-76;
tive 28; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 62.63
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; US-10-442-148A-7
RESULT 1
US-10-442-148A-7
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QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
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                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/10121258
; Publication No. US20030059835A1
; GENERAL INFORMATION:
; APPLICANT: Traien, Roger
; APPLICANT: Traien, Roger
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
; TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
; TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
; FILE REFERENCE: UC083.1CP2CP1
; CURRENT APPLICATION NUMBER: 09/794,308
; PRIOR FILING DATE: 2001-02-26
; PRIOR PILING DATE: 2001-02-26
; PRIOR PILING DATE: 2001-02-24
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FESLESQ for Windows Version 4.0
; SEQ ID NO 20
                                                                                                                                                                     14;
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                                                                                                                         Length 225;
                                                                                                                                                                   Indels
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                                                   ; OTHER INFORMATION: variant of sequence from Discosoma sp. US-10-315-920-6
                                                                                                                  Query Match 61.7%; Score 782; DB 14;
Best Local Similarity 62.6%; Pred. No. 2.7e-76;
Matches 144; Conservative 28; Mismatches 44;
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61.6%; Score 781; DB 14;
Best Local Similarity 62.6%; Pred. No. 3.5e-76;
Matches 144; Conservative 28; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: DsRed with I125R
       ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                              APPLICANT: IWAKURA, MASAHIRO
APPLICANT: HIROTA, KIYONORI
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ORIENTATION-CONTROLLED PROTEIN AND
TITLE OF INVENTION: PROCESS FOR ARRAYING AND IMMOBILIZING PROTEIN USING THE SAME
FILE REFERENCE: 04583.0103-00000
CURRENT PAPLICATION NUMBER: US/10/442,148A
CURRENT FILING DATE: 2003-05-21
PRIOR FILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
  126 GVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGETHKALKLKDGGHYLVEFKSIYMAKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
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                                          181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRVKSRH 230
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APPLICANT: Fradkov, Alexey
TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS
TITLE OF INVENTION: FOR THEIR USE
FILE REFERENCE: CLON-077CIP
CURRENT APPLICATION NUMBER: US/10/315,920
CURRENT APPLICATION NUMBER: 05/211,607
PRIOR APPLICATION NUMBER: 60/211,607
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FRASEQ for Windows Version 4.0
                                                                      Sequence 8, Application US/10442148A Publication No. US20040014242A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 6, Application US/10315920
; Publication No. US20030175809A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                     RESULT 2
US-10-442-148A-8
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LENGTH: 27
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ORGANISM: Artificial
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US-10-314-936-4
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| Publication No. US20040110225A1
| GENERAL INFORMATION:
| APPLICANT: Gibbs. Patrick D.L.
| APPLICANT: Schmale, Michael C.
| TITLE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPECIES
| FILE REPERENCE: 20004
| CURRENT FILING DATE: 2002-12-09
| NUMBER OF SEQ ID NOS: 15
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 2.
| LENGTH: 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRVKSRH 230
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Sequence 4, Application US/10315920

Sequence 4, Application US/10315920

Bublication No. US20030175809A1

GENERAL INFORMATION:

APPLICANT: Frackov, Arcady Fedorovich

APPLICANT: Frackov, Arcady Fedorovich

APPLICANT: Frackov, Arcady Fedorovich

TITLE OF INVENTION: FUUGRESCENT TIMER PROTEINS AND METHODS

TITLE OF INVENTION: FOR THEIR USE

FILE REFERENCE: CLON-077CIP

CURRENT APPLICATION NUMBER: US/10/315,920

CURRENT FILING DATE: 2002-12-09

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2001-06-13

PRIOR FILING DATE: 2001-06-13

NUMBER OF SEQ ID NOS: 22

SEQ ID NO 4

SEQ ID NO 4.
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; OTHER INFORMATION: mutant red fluorescent protein US-10-314-936-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.6%; Score 781; DB 14; 62.6%; Pred. No. 3.5e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28; Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 62.6
Matches 144; Conservative
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Matches 144:
US-10-315-920-4
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Best Local
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61 OYGSIPFTKYPEDIPDYVKOSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
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                                                                 6 NVIKEFMRFKVRMEGTVNGHBFEIEGEGERPYEGHNTVKLKVTKGGPLPFAMDILSPOF
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Sequence 67, Application US/09999745
Batent No. US20020157120A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Taien, Roger Y.
APPLICANT: Taien, Conferey
TITLE OF INVENTION: CIRCULARILY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: REGEN1470-1
CURRENT PAPLICATION UNBER: US/09/999,745
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/316,920
SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gibbs, Patrick D.L.
APPLICANT: Garter, Robert W.
APPLICANT: Schmale, Michael C.
APPLICANT: Schmale, Michael C.
APPLICANT: Schmale, Michael C.
APPLICANT: Schmale, Michael C.
TITLE OF INVENTION FUNDRESCENT PROTEINS FROM AQUATIC SPECIES
FILE REFERENCE: 638.004
CURRENT APPLICATION NUMBER: US/10/314,936
CURRENT FILING DATE: 2020-12-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 PVQLPGYYYVDSKLDITSHNKDYTIVEQYE---
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61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
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; Sequence 12, Application US/09865291
; Publication No. US20030186229A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSIEN, ROGER
; APPLICANT: TING, Alice
; APPLICANT: TING, Alice
; APPLICANT: EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
; TITLE OF INVENTION: EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
; FILE REFERENCE: REGENISSON
; CURRENT APPLICATION NUMBER: US/09/865,291
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PATENTIN VERSION 3.0
; SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
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          Sequence 12, Application US/09794308
PUblication No. US20030170911A1
GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGER
APPLICANT: APPLICANT: David
APPLICANT: APPLICANT: APPLICANTS, David
APPLICANT: BAIRD, GOOFFERS, David
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
CURRENT APPLICATION NUMBER: US/09/794,308
CURRENT PILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Indels
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62.6%; Pred. No. 4.4e-76;
ive 28; Mismatches 44;
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Best Local Similarity 62.6%; Pred. No. 4.4e-76;
Matches 144; Conservative 28; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 PVQLPGYYYVDSKLDITSHNEDYTIVEQYE----
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.64
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Discosoma sp.
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US-09-66-538-12

Sequence 12, Application US/09866538

Publication No. US20030032088A1

GENERAL INFORMATION:
APPLICANT: TSIEN, ROGER

APPLICANT: TSIEN, ROGER

TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: REGENIS30-2

CURRENT APPLICATION NUMBER: US/09/866,538

CURRENT FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 12

FERMIN OF SECULIA VERSION 3.0
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62.6%; Pred. No. 4.4e-76;
tive 28; Mismatches 44
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62.6%; Pred. No. 4.4e-76;
iive 28; Mismatches 44;
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                   Query Match
Best Local Similarity 62.6*
Matches 144; Conservative
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Best Local Similarity 62.6
Matches 144, Conservative
                                                                                                   TYPE: PRT

ORGANISM: Discosoma sp.
US-09-999-745-67
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; ORGANISM: Discosoma sp.
US-09-866-538-12
                                                              SEQ ID NO 67
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RESULT 10 US-09-794-308-12

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PRIOR APPLICATION NUMBER: 09/458,144
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 225
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                                                                                                                                                                                                                                                                                                          ORGANISM: Discosoma species US-10-006-922-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 62.6%
Matches 144; Conservative
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Matches 144; Conservative
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TYPE: PRT
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Sequence 12, Application US/10006922

Redication No. US20020197676A1

GENERAL INFORMATION:
GENERAL INFORMATION:
Fradkov, Arcady F.
APPLICANT: Labas, Yulii A.
APPLICANT: Labas, Yulii A.
APPLICANT: Marz, Mikhail V.
APPLICANT: Marz, Mikhail V.
APPLICANT: Marz, Mikhail V.
APPLICANT: Marz, Mikhail V.
APPLICANT: Marz, Mikhail V.
APPLICANT: Marz, Mikhail V.
APPLICANT: Marz, Mikhail V.
APPLICANT: Marz, Mikhail V.
APPLICANT: Marz, Mikhail V.
FILE REFERENCE: CLON-035CIP
CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT APPLICATION NUMBER: US/120,330

PRIOR FILING DATE: 1998-12-11

PRIOR FILING DATE: 1998-12-09
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         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
                               GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
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Binding Ligands With Intrinsic
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                                                                                                   181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRVKSRH 230
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                                                                                                                                            ---RTEGRH 221
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US-10-132-067-4
                                                                                                                                                                                                                                                                                                                        APPLICANT: Bradbury, Andrew
APPLICANT: Zeytun, Ahmet
APPLICANT: Zeytun, Ahmet
APPLICANT: Waldo, Geoffrey
TYTLE OF INVENTION: Fluorobodies: Binding Li
TITLE OF INVENTION: Fluoroscence
FILE REFERENCE: 021362-000660US
CURRENT APPLICATION NUMBER: US/10/132,067
CURRENT FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 48
SEQ ID NO 4
LENGTH: 225
                                                                                                                           186 PVQLPGYYYVDSKLDITSHNEDYTIVEQYE
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                                                                                                                                                                                                                                                       Sequence 4, Application US/10132067 Publication No. US20030203355A1 GENERAL INFORMATION:
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Best Local Similarity 62.61
Matches 144; Conservative
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ORGANISM: Discosoma sp.
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APPLICANT: Lukyanov, Sergey
APPLICANT: Lukyanov, Konstantin
APPLICANT: Lukyanov, Konstantin
APPLICANT: Savistky, Alexandr
APPLICANT: Savistky, Alexandr
APPLICANT: Fradkov, Arcady
TITLE OF INVENTION: No. US20030022287Al Aggregating Fluorescent Proteins and
TITLE OF INVENTION: Methods for Using the Same
TITLE OF INVENTION: Methods for Using the Same
FILE REFERENCE: CLON-067
CURRENT FILING DATE: 2002-06-19
FRIOR APPLICATION NUMBER: 10/006,922
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                         66 QYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
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                                                                                                                      1 SVIAKOMIYKVYMSGTVNGHYFEVEGDGKGKPYBGEQTVRLAVTKGGPLPFAWDILSPQC
                                                                                                                                                     6 NVIXEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAMDILSPQF
                                                                                                                                                                                                                                             61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
                                                                                                                                                                                                                                                                                                                                                          121 GINFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRVKSRH 230
                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----RTEGRH 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels 14;
61.5%; Score 780; DB 13; Length 225; 62.6%; Pred. No. 4.4e-76; cive 28; Mismatches 44; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 225;
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62.6%; Pred. No. 4.4e-76;
live 28; Mismatches 44;
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GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFWALKLEGGGHYLCEFKSTYKARK 180
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Best Local Similarity 62.6%; Pred. No. 4.4e-76;
Matches 144; Conservative 28; Mismatches 44; Indels 14; Gaps
                                                                                                                                                                                                                                                                  Sequence 1, Application US/10121258
; Publication No. US20030059835A1
; GRNERAL INFORMATION:
; APPLICANT: Tsien, Roger
APPLICANT: Tsien, Roger
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; TITLE OF INVENTION: PROTERT VARIANTS AND METHODS FOR MAKING SAME
; TITLE OF INVENTION: MONOMERIC AND JUMERIC FLUORESCENT
; TITLE OF INVENTION: MONOMER: US/10/121,258
; CURRENT APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/866,538
; NUMBER OF ESC ID NOS: 78
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
: LENGTH: 225
                                                                                                                                       181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRVKSRH 230
                                                                                                                                                                                -----RTEGRH 221
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-----RTEGRH 221
                                                                                                                                                               Search completed: August 12, 2004, 06:51:21 Job time : 487.141 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(225)

OTHER INFORMATION: wild-type DsRed
US-10-121-258-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Discosoma sp.
                                                                                                                                                                                                                                       RESULT 15
US-10-121-258-1
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2004, 06:12:47; Search time 24.1414 Seconds (without alignments) 493.990 Million cell updates/sec

Le: US-09-890-463-3

Perfect score: 1268 Sequence: 1 SVIAKQMTYKVYMSGTVNGH......SIARKPLVACCFFRVKSRHK 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

...um DB Seq Length: Z000000000 -processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

lssued_Patents_AA:*

1. \( \cgn^2 \) \( \chi \text{CoMB.pep:*} \)

2. \( \cgn^2 \) \( \chi \text{Codata} / 2 \) \( \text{Laa} / 5 \)

3. \( \cgn^2 \) \( \chi \text{Codata} / 2 \) \( \text{Laa} / 6 \)

4: \( \cgn^2 \) \( \chi \text{Codata} / 2 \) \( \text{Laa} / 6 \)

4: \( \cgn^2 \) \( \chi \text{Logata} / 2 \) \( \text{Laa} / 6 \)

5: \( \cgn^2 \) \( \chi \text{Logata} / 2 \) \( \text{Laa} / 2 \) \( \text{Laa} / 2 \)

6: \( \cgn^2 \) \( \chi \text{Logata} / 2 \) \( \text{Laa} / 2 \) \( \text{Laa} / 2 \) \( \text{Laa} / 2 \)

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTE

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	Description	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	
		! ! !																										
SUMMARIES		277-716-16	609-1	626-5	415	626-580C-65	277-716-32	609-161B-32	839-620-3	472-0	479	023-946B-28	023-	023-946B-36	9-129-192C-49	9-023-946B-22	337-	753-	619-	98	792-5	893-327-16	753-14	094-35	-172-063-2	21-53	-263-975-2	
Mins	ID	-60-SN	-60-SD	-60-SD	US-09-	-60-SD	-60-SD	-60-SD	-60-SD	-60-	-60-SD	US-09-	-60-SN	-60-SD	-60-Sn	-60-SD	US-08-	0	-08-	US-08-	-08-	US-08-	US-08-	0	-60-SN	-60-SD	-60-SN	
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	Length	238	238	238	238	. 238	238	238	238	238	238	238	238	238	240	238	238	238	238	238	238	238	238	238	238	238	238	
de	Query Match	38.1	38.1	38.1	38.1	38.1	37.3	37.3	37.2		15.2	15.1	14.9	14.9	14.9	14.8	٠	•	•	14.8	•	14.8	14.8	14.8	14.8	14.8	14.8	
	Score	482.5	482.5	•	482.5	482.5		473.5			192.5	•		188.5		188				187.5						187.5		
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RESULT 2 US-09-609-161B-16

٦,	Sequence 2, Appli	Sequence 10, Appl	Sequence 159, App	Sequence 2, Appli	74,	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 29, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	4	m	7	Sequence 46, Appl
US-09-418-785-1	US-09-214-909-2	US-09-479-645A-10	US-09-479-645A-159	US-09-129-192C-2	US-09-129-192C-74	US-09-602-641-2	US-09-704-463-2	US-09-472-065A-4	US-09-472-065A-6	US-09-023-946B-29	US-09-920-922-4	PCT-US95-14692-2	US-08-646-538-2	US-09-094-359-4	US-09-172-063-3	US-09-503-222-2	US-09-513-783A-46
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238	238	238	238	238	238	238	238	238	238	238	238	238	239	239	239	239	239
14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8
187.5	187.5	187.5	187,5	187.5	187.5	187.5	187.5	187.5	187.5	187.5	187.5	187.5	187.5	187.5	187.5	187.5	187.5
28	5	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 FTKYPEDIPDYVKQSFPGRYTWBRIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 NGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGGHYLCEFKSTYKARKPVK-MP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 MSYKVNLEGIVNNHVFTMEGCGKGNILFGNQLVQIRVTKGAPLPFAFDIVSPAFQYGNRT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 MIYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; CTHER INFORMATION: Renilla mulleri Green Fluorescent Protein (GFP) US-09-277-716-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.1%; Score 482.5; DB 3; Length 238; 44.0%; Pred. No. 2.2e-45; tive 41; Mismatches 74; Indels 7
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APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LID.
TITLE OF INVERTION: LUCIFERASES, FLUORESCENT
CURRENT APPLICATION NUMBER: US/09/277,716A
CURRENT APPLICATION NUMBER: 60/102,939
EARLIER APPLICATION NUMBER: 60/102,939
EARLIER FILING DATE: 1998-10-01
EARLIER PLING DATE: 1998-06-15
EARLIER PLING DATE: 1998-06-15
EARLIER PLING DATE: 1998-06-15
EARLIER PLING DATE: 1998-06-15
EARLIER FILING DATE: 1998-06-15
EARLIER PLING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
Sequence 16, Application US/09277716A Patent No. 6232107
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 44.0%
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Renilla mulleri
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Sequence 65, Application US/09626580C
Batent No. 6562617
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Begenberger, Jakob M.
APPLICANT: Peele, Beau R.
APPLICANT: Peele, Dean R.
TITLE OF INVENTION: FUSIONS OF SCAFFOLD PROTEINS WITH RANDOM PEPTIDE LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 FTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPP 126
                                                                                                                                                                                                                                                                                                                    67 FTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPP 126
                                                                                                                                                                                                                                                                                                                                                     NGPVMQKKTQGWEPNTERLFARDGMLJGNNFMALKLEGGGHYLCEFKSTYKARKPVK-MP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 FTKYPNDISDYPIOSFPAGFMYERTLRYEDGGLVEIRSDINLIEDKFVYRVEYKGSNFPD 134
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                                                                                                                                                                                                                    15 MSYKVNLEGIVNNHVFTMEGCGKGNILFGNQLVQIRVTKGAPLPFAFDIVSPAFQYGNRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 65, Application US/09415765B
Sequence 65, Application US/09415765B
Patent No. 654662
GRNERAL INFORMATION:
APPLICANT: Anderson. David
TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide
TITLE OF INVENTION: Libraries
TITLE OF INVENTION: Libraries
TITLE OF INVENTION: Libraries
CURRENT APPLICATION NUMBER: US/09/415,765B
CURRENT FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 09/169,015
PRIOR PLING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 238;
                                    Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 SYHFIQHRLEKT-YVEDGGFVEQHETALAQMTSIGKPL 231
                                 ; Score 482.5; DB 4;
; Pred. No. 2.2e-45;
41; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.1%; Score 482.5; DB 4; Best Local Similarity 44.0%; Pred. No. 2.2e-45; Matches 96; Conservative 41; Mismatches 74;
                                    38.18;
44.08;
                                                                                                      96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Renilla muelleri
US-09-415-765B-65
                                                          Best Local Similarity Matches 96; Conserv
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US-09-626-580C-65
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LENGTH: 238
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                                                                                APPLICANT: BITCHARLIANS,
APPLICANT: BYAH, BITCHE
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROTUME, LID.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIC
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE BEFERENCE: 24729-121B
CURRENT APPLICATION NUMBER: US/09/609,161B
CURRENT APPLICATION NUMBER: 00/0-6-30
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-06-10-1
PRIOR FILING DATE: 1999-0-10-1
PRIOR FILING DATE: 1999-0-6-15
PRIOR FILING DATE: 1999-0-6-15
PRIOR FILING DATE: 1999-0-6-15
PRIOR FILING DATE: 1999-0-6-15
PRIOR FILING DATE: 1999-0-6-15
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Fatent No. 6548249
GENERAL INFORMATION:
TITLE OF INVENTION: Lubraries
TITLE OF INVENTION: Libraries
TITLE OF INVENTION UNMBER: US/09/626,581D
CURRENT FILING DATE: 2000-07-27
FRICH APPLICATION NUMBER: 09/15,015
FRICH FILING DATE: 1999-10-08
FRICH FILING DATE: 1999-10-08
FRICH FILING DATE: 1999-10-08
FRICH FILING DATE: 1999-10-08
FRICH FILING DATE: 1999-10-08
FRICH FILING DATE: 1099-10-08
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; ORGANISM: Renilla muelleri
US-09-626-581D-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 44.0<sup>o</sup>
Matches 96; Conservative
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US-09-626-581D-65
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TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUCITITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUCITITLE OF INVENTION: SCREENING AND NOVELTY ITEMS

TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS

FILE REPERENCE: 24729-1218

CURRENT APPLICATION NUMBER: US/09/609,161B

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-01-01

PRIOR FILING DATE: 1998-00-15

PRIOR FILING DATE: 1998-06-15

PRIOR FILING DATE: 1998-06-15

PRIOR FILING DATE: 1998-06-15

PRIOR FILING DATE: 1998-06-15
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Patent No. 645761
GENERAL INCRMATION:
APPLICANT: Stratagene
TITLE OF INVENTION: Humanized Polynucleotide Sequence Encoding Renilla Mulleri Green
Patent No. 6645761
TITLE OF INVENTION: Fluorescent Protein
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                      75 FTKYPDDIADYFVQSFPAGFFYERNLRFEDGAIVDIRSDISLEDDKFHYKVEYRGNGFPS 134
                                                                  127 NGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARKPVK-MP 185
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                                                                                                                                                                186 GYHYVDRKLDVTNHNKDYTSVEQREISIAR-----KPL 218
                                                                                                                                                                                           APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
                                                                                                                                                                                                                                                                                                                         Sequence 32, Application US/09609161B Patent No. 6436682
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Best Local Similarity
Matches 96; Conservi
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US-09-609-161B-32
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APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LICTERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
CURRENT PILING DATE: 1999-03-26
EARLIER PILING DATE: 1999-03-26
EARLIER PILING DATE: 1998-10-01
EARLIER PILING DATE: 1998-06-15
EARLIER PILING DATE: 1998-06-15
EARLIER PILING DATE: 1998-06-15
EARLIER PILING DATE: 1998-03-27
SARIER APPLICATION NUMBER: 60/079,624
EARLIER FILING DATE: 1998-03-27
SOFTWARE: PATENTION OF: 2.0
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; OTHER INFORMATION: Ptilosarcus gurneyi Green Fluorescent Protein (GFP)
US-09-277-716-32
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FILE REFERENCE: A-66900-2/RMS/AMS
CURRENT APPLICATION NUMBER: US/09/626,580C
CURRENT FILING NATE.
                                                             CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 65
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ORGANISM: Ptilosarcus gurneyi
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Matches 96; Conserv
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                                                                                                                                                                                                             Gaps
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                                                                                                                                                                              Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Evans, Krista
TITLE OF INVENTION: Mutants of Green Fluorescent Protein
FILE BEFERENCE: 0942.402002
CURRENT APPLICATION NUMBER: US/09/472,065A
CURRENT FILING DATE: 1999-12-23
FRIOR FILING DATE: 1997-11-14
FRIOR FILING DATE: 1997-11-14
FRIOR FILING DATE: 1997-11-15
SRIOR FILING DATE: 1997-11-15
SRIOR PRIJOR OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5.
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   218
                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.2%; Score 471.5; DB 4;
43.6%; Pred. No. 3.7e-44;
iive 40; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                  186 GYHYVDRKLDVTNHNKDYTSVEQREISIAR----KPL
FILE REFERENCE: 25436/1755
CURRENT APPLICATION NUMBER: US/09/839,650
CURRENT FILING DATE: 2001-04-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 3
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PVLLPDNHYLSTOSALSKDPNEKRDH 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-472-065A-5
; Sequence 5, Application US/09472065A
...ant No. 6638732
                                                                                                                                                                         Query Match
Best Local Similarity 43.68
Matches 95; Conservative
                                                                                                             TYPE: PRT ORGANISM: Renilla muelleri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53; Conservative
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Best Local Similarity
Matches 53; Conserv
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                                                                                                                                      US-09-839-650-3
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71 PEDIP--DYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNG 128
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TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AND METHOD FOR SELECTIVELY
TITLE OF INVENTION: EXPRESSING A PROTEIN IN A TARGET CELL OR TISSUE
FILE REFERENCE: 210338.0001/102
CURRENT APPLICATION NUMBER: US/09/479,645A
CURRENT FILING DATE: 2000-01-07
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1997-07-09
PRIOR PILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 219
SOUTHMER: Patentin Ver. 2.0
SEQ ID NO 12
THE OFFICE TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOTES TOWN NOT
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Patent No. 6670449
GENERAL INPORMATION:
APPLICANT: GERO MIESENBOCK, ET AL.
APPLICANT: GERO MIESENBOCK, ET AL.
TITLE OF INVENTION: HYBRID MOLECULES AND
THEIR USE FOR OPTICALLY DETECTING CHANGES IN
CELLULAR MICROENVIRONMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic gfp
OTHER INFORMATION: gene (Papillomavirusized)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.2%; Score 192.5; DB 4; Length 238; 25.2%; Pred. No. 3.4e-13; tive 47; Mismatches 90; Indels 17
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OTHER INFORMATION: Codons of humanized gfp gene replaced with
OTHER INFORMATION: synonymous codons used at relatively high
OTHER INFORMATION: frequency by papillomavirus genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSER. MOGGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
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PVLLPDNHYLSTOSALSKDPNEKRDH 217
RESULT 10
US-00-479-645A-12
; Sequence 12, Application US/09479645A
; Patent No. 6489141
; GRNERAL INFORMATION:
; APPLICANT: FRAZER, Ian Hector
; APPLICANT: ZHOU, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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71 PEDIP--DYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNG 128
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TITLE OF INVENTION: HYBRID MOLECULES AND
THEIR USE FOR OPTICALLY DETECTING CHANGES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
14.9%; Score 189.5; DB 4; Length
Best Local Similarity 26.2%; Pred. No. 7.3e-13;
Matches 54; Conservative 44; Mismatches 91; Indels
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                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,285
REFERENCE/DOCKET NUMBER: 2955-4004US2
TELECOMMUNICATION INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/023,946B
FILING DATE: 13-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,805
FILING DATE: 14 FEBRUARY 1997
APPLICATION NUMBER: 60/038,179
FILING DATE: 13 FEBRUARY 1997
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,946B
FILING DATE: 13-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: UNKNOWN SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 PVLLPDNHYLHTQSALSKDPNEKRDH 217
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ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                            NAME: KENNETH H.SONNENFELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36, Application US/09023946B Patent No. 6670449 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
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Patent No. 6670449
GENERAL INFORMATION:
APPLICANT: GERO MISSENBOCK, ET AL.
TITLE OF INVENTION: HYBRID MOLECULES AND
THEIR USE FOR OPTICALLY DETECTING CHANGES IN
CELLULAR MICROENVIRONMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 15.1%; Score 191.5; DB 4; Length 238; Local Similarity 25.7%; Pred. No. 4.4e-13; les 53; Conservative 46; Mismatches 90; Indels 17;
                                                                                                                                                                                                                                              FILING DATE: 14 FEBRUARY 1997
APPLICATION WUNBER: 60/038,179
FILING DATE: 13 FEBRUARY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KENNETH H.SONNENFELD
REGISTRATION NUMBER: 33,285
REFERENCE/DOCKET NUMBER: 2955-4004US2
                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,946B
FILLING DATE: 13-Feb-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: UNKNOWN SEQ ID NO: 28: US-09-023-946B-28
                                                                                                                                                                                                                              APPLICATION NUMBER: 60/036,805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 PVKMPGYHYVDRKLDVT---NHNKDY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | : | | : | : | : | : | | PVLLPDNHYLHTQSALSKDPNEKRDH 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 756-4800
TELEFRAX: (212) 751-6849
TELERAX: 421792
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                       FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID STRANDEDNESS: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 PVMQKKTQGWEPNTERLF----ARDGMLIGNNF-MALKLEGGGHYLCEF--KSTYKARK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: | :: | :: | :: | 135 NILGHKLE-YNYNDHQVYIMADKQKNG--IKANFKIRHNIEDGGGVQLADHYQQNTPIGDG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
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                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/09023946B

Patent No. 6670449

GENERAL INFORMATION:
APPLICANT: GERO MIESENBOCK, ET AL.

TITLE OF INVENTION: HYBRID MOLECULES AND
THEIR USE FOR OPTICALLY DETECTING CHANGES IN
CELLULAR MICROENVIRONMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                   180 LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDH 219
                                                                                         --PVKMPGYHYVDRKLDVT---NHNKDY
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APPLICATION NUMBER: US/09/023,946B
FILING DATE: 13-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,805
FILING DATE: 14 FEBRUARY 1997
APPLICATION NUMBER: 60/038,179
FILING DATE: 13 FEBRUARY 1997
ATTONNEY/AGENT INFORMATION:
NAME: KENNETH H.SONNENFELD
REGISTRATION NUMBER: 33,285
REFERENCE/DOCKET NUMBER: 2955-4004US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.8%; Score 188; DB 4; 27.4%; Pred. No. 1.1e-12; iive 39; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
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TOPOLOGY: UNKNOWN

SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-023-946B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
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137 NILGHKLE-YNYNSHKVY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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Best Local Similarity 27.4%
Matches 52, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF
                                                                                                                                                                                                                                                       RESULT 15
US-09-023-946B-22
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APPLICANT: Aurora Biosciences Corporation
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
FILE REFERENCE: AUROL270 (10836/09/1291)
CURRENT APPLICATION NUMBER: US/09/1291)
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.0
SEQ ID NO 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 VELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTT-GKLPVPWPTLVTTFSYGVQCFSRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 PEDIP--DYVKOSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 PDHMKRHDFFKSAMPEGYVQERTIFPKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.9%; Score 188.5; DB 4; 25.9%; Pred. No. 9.5e-13; iive 45; Mismatches 92;
                APPLICATION NUMBER: 60/038,179
FILING DATE: 13 FEBRUARY 1997
ATTORNEY/AGENT INPORMATION:
NAME: KENNETH H.SONNENFELD
REGISTRATION NUMBER: 33,285
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.9%; Score 188.5; DB 4
23.6%; Pred. No. 9.6e-13;
live 41; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-023-946B-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKMPGYHYVDRKLDVT---NHNKDY 203
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FILING DATE: 14 FEBRUARY 1997
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                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 23.6%; 52; Conservative 4
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                                                                                                                                                                                                                                                                                                                      TELEX: 421792
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ORGANISM: GFP
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Search completed: August 12, 2004, 06:21:06 Job time : 25.1414 secs

COOST AND BOOK SILL

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

August 12, 2004, 06:12:47; Search time 21.6701 Seconds (without alignments) 1043.144 Million cell updates/sec

US-09-890-463-4 1287 1 SVIAKQMTYKVYMSGTVNGH......KPVVACRFFRVKSRHKYAVA 235 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AB0124	S26373	872350	F90399	863985	E69895	S19676	AC2239	CDPJ25	I55184	A60154	E65045	H84385	P2IVBS	S14939	A42013
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77.5	77.5	77.5	77	77	76.5	76.5	76.5	16	16	16	2/	26	26	16	75.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1  GD1144  GD1144  GD1144  GD1144  GD1144  GD1144  GD1144  GD1144  GD1144  GD1144  GD1144  GD1144  GD1144  GD1144  GD1144  GD1144  GD1145  GD1145  GD1145  GD1155  GD1159  GD1145  GD1159  GD1145  GD1159  GD1145  GD1159  GD1145  GD1159  GD1145  GD1159  GD1145  GD1159  GD1145  GD1159  GD1145  GD1159  GD1145  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD1159  GD11
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A,Molecule type: DNA
A,Residues: 1-368 <PAR>
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N;Alternate names: hypothetical protein 12349
C;Species: Caccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2002
C;Accession: S64909
R;Pohl, T.M.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64899
A;Mccession: S64909
A;Mccession: S64909
A;Reference number: S64899
A;Mccession: S64909
A;Mccession: S64909
A;Mccession: S64909
A;Coss-references: EMBL:Z73249; NID:g1360436; PID:e245794; PID:g1360437; GSPDB:GN00012;
A;Experimental source: strain $288C
C;Genetics:
A;Gene: MIPS:YLR077w
A;Cross-references: SGD:S0004067
A;Map position: 12R
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YLR077w
C;Keywords: transmembrane protein
F;81-97/Domain: transmembrane #status predicted <TWM>
A;Contents: annotation; X-ray crystallography, 1.9 angstroms
C;Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittin C;Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Cenemics: 69/3; 167/3
A;Introns: 69/3; 167/3
C;Superfamily: green-fluorescent protein
C;Keywords: chromoprotein; luminescence
F;65-67/Cross-link: 5-imidazolinone (Ser-Gly) #status experimental
F;66/Modified site: dehydrotyrosine (Tyr) #status experimental
                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                              71 PEDIP--DYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVMQKKTQGWEPNTERLF-----ARDGMLIGNNF-MALKLEGGGHYLCEF--KSTYKAKK 180
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                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                     Length 238;
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                                                                                                                                                                                                                                14.4%; Score 185.5; DB 1
24.8%; Pred. No. 4.9e-09;
live 47; Mismatches 91
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hypothetical protein Cj1433c [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: A81289
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: GB:AL1139078, GB:AL11168; NID:g6968723, PIDN:CAB73857.1, PID:g696886
A,Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unthranilate synthase multifunctional protein - Aspergillus niger
NyAlternate names: gene trpG-trpC-trpF protein; glutamine amidotransferase
NyContains: anthranilate synthase (EC 4.1.3.27); indole-3-glycerol-phosphate synthase (EC 5;Species: Aspergillus niger
C;Species: Aspergillus niger
C;Date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text_change 31-Mar-2000
C;Accession: S00643; A23979; E23979
R;Kos, T: Kuijvenhoven, A: Hessing, H.G.M.; Pouwels, P.H.; van den Hondel, C.A.M.J.J.
Curr. Genet. 13, 137-144, 1988
A;Title: Nucleotide sequence of the Aspergillus niger trpC gene: structural relationship
A;Reference number: S00643; MUD:88223483; PMID:2836085
A;Residue type: DNA
A;Residues: 1-770 cxos>
A;Residues: 1-770 cxos>
A;Residues: 1-770 cxos>
A;Cross-references: ERMEL:X07071; NID:92420; PIDN:CAA30107.1; PID:92421
B;Kos, A.; Kuijvenhoven, J.; Wernars, K.; Bos, C.J.; van den Broek, H.W.J.; Pouwels, P.H.
Gene 39, 231-238, 1985
A;Reference number: A91539; WUID:86137391; PMID:2936650
--DHGOLGIGKKTMKCAKPMNIPEVLKPGODTTD--LDSIYN 559
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A;Residues: 1-69 <KO2>
A;Cross-references: GB:M14404; NID:g166536; PIDN:AAA32709.1; PID:g166537
A;Accession: B22979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: Cj1433c
C,Superfamily: Campylobacter jejuni hypothetical protein Cj1433c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.7%; Score 86.5; DB 2;
21.9%; Pred. No. 5.1;
tive 22; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: :| ||
227 PIKINWDLIKDKCDQY-----DIP--
                                                                                                                                                              583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 SLDPSGNCDNYH---SFTNCSMANHCVQFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --KSRHKYAV
                                                                                 200 NKDYTSVEQCEISIARKPVVACRFFRV
                                                                                                                                     SEO SKLHLKKEQRVVTNGNK---SCLYWRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 NKKYGNHFEVCEFDFIDIYKA
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m

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C;Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane F
11-19/Domain: signal sequence #status predicted <SIG>
F)1-29/Domain: immunoglobulin homology <IMM1>
F)13-191/Domain: immunoglobulin homology <IMM2>
F)13-191/Domain: immunoglobulin homology <IMM2>
F)15-156/Region: heparin binding #status predicted
F)161-165/Region: heparin binding #status predicted
F)263-272/Region: nCAM binding #status predicted
F)263-272/Region: NCAM binding #status predicted
F)263-272/Region: nCAM binding #status predicted
F)263-272/Region: immunoglobulin homology <IMM4>
F)420-482/Domain: immunoglobulin homology <IMM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MJID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-797 <HEI>
A;Cross-references: GB:AE004131; GB:AE003852; NID:g9654856; PIDN:AAF93619.1; GSPDB:GN0012
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organic solvent tolerance protein VC0446 [imported] - Vibrio cholerae (strain N16961 serc
                                                                                                                                                                                                                                                                                                                          F;519-596/Domain: fibronectin type III repeat homology <FN3A>
F;625-685/Domain: fibronectin type III repeat homology <FN3B>
F;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F;212,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 SPQCQYGSIPFIKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 QGNCFI-----YHVKFSGLNFPPNGPVMQ---KKTQG----WEPNTERLFARDGMLI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: E82323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 ----QCQY-----GSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 ÓLSYNYYAPETMKYLDLDLVSHVSRFETDARGKP----SATRVHIEPGLKIPFSNTWGNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 KVYMSGTVNGHYFEVEGDGKGK--PYE-----GEQTVR-LAVIKGGPLPFAWDILSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---AKEANM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 OMTYKVYMSGTVN-----GHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFA--WDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 GNNFMALKLEGGG----HYLCEFKSTYKAKKP-VKMP-GYHYVDRKLDVTNHNKDY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           619 KVNL--IKQDDGGSPIRHYLVKYRALASEWKPEIRLPSGSHHV--MLKSLDWNAEY 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444 TTEAR---VLGTYYQQDLDKTTD-----AKLEESVTRVIPEIRSV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----RDGMLIGNNFMAL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | |: ::|: :||
513 SSTAQVQFDEPEATGGVPILKYKAEWKSLGEESW--HFTWYD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 1
C;Superfamily: organic solvent tolerance protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.5%; Score 84;
2.9%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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oxo-aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse N;Alternate names: NCM-120 C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 31-Mar-1993 #text_change 31-Dec-2000 C;Accession: A29673; S00382; A44290 R;Barthels, D:; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fonted A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000 A;Reference number: A29673; MUID:87246524; PMID:3595563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJMS
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                                                                                                                                                              C;Superfamily: trpG-trpC-trpF trifunctional enzyme; trpC homology; trpF homology; trpG S;Reywords: carbon-carbon lyase; carboxy-lyase; intramolecular lyase; isomerase; oxo-ac F;25-219/Domain: glutamine amidotransferase #status predicted <GAT>
F;26-216/pomain: trpG homology <TRG>
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A; Residues: 1-725 <BAR>
A; Cross-references: EMB:Y00051; NID:953342; PIDN:CAA68263.1; PID:953343
R; Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A; Title: Differential splicing and alternative polyadenylation generates distinct NCAM
A; Reference number: S00382; MUID:88283628; PMID:3396534
                                                                                                                                                                                                                                                                                           F;255-518/Domain: trpC homology <TRC>
F;255-514/Domain: indole-3-glycerol-phosphate synthase #status predicted <IGPS>
F;257-767/Domain: trpP homology <TRP >
F;537-767/Domain: homology <TRP >
F;545-770/Domain: M-(5'-phosphoribosyl) anthranilate isomerase #status predicted <PRAI>
F;104/Active site: Cys #status predicted
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A; Residues: 642-656, D', 658-725 <BA2>
A; Cross-references: EMBL:X07195
R; Rougon, G.; Marshak, D.R.
J. Blod. Chem. 261, 3396-3401, 1986
A; Title: Structural and immunological characterization of the amino-terminal domain
A; Reference number: A44290; MUID:86140120; PMID:3512556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYPE-----DIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS-- 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ESILTEYGRIMFRNFLKLTAGTWEGNGKHFGEQSSTTK 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 KVYMSGTV-NGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFT
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A,Molecule type: DNA
A,Residues: 392-433 <KO3>
A,Cross-references: GB:M14403; NID:g166538; PIDN:AAA32710.1; PID:g166539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.7%; Score 86; DB 2; Length 770;
24.3%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.3%; Pred. 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 ATVPSNPP--PKTDKKLSILERIYDH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 20-36 < ROU>
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A; Introns: 701/1
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Matches
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Db 481AGIVLERDTVLLDDYTQTLEPKIQYLYVPEKXQDNIGLYDSTLLQTDYYGLFRSRKY 537	Matches 52; Conservative 40; Mismatches 80; Indels 56; Gaps 14;
QY 161KLEGGGHYLCEFKSTYKAKKPVKMPGYHYVDRKLDVTNHNKDYTS 205 ::	QY 31 KPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPGRYTWER 90   :-
RESULT 7 B70419 hypothetical protein aq 1369 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: Aquifex aeolicus C;Accession: 1998 #sequence_revision 08-May-1998 #text_change 04-Mar-2000 C;Accession: B70419 R;Deckert, G.; Marren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov	91 IMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQ)
Vature 392, 353-358, 1998  A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: B70419 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Abccule type: DA A;Cross-references: GB:AE000737; NID:g2983782; PIDN:AAC07356.1; PID:g2983798; GB:AE00065 A;Experimental source: strain VFS C;Genetics: A;Gene: aq_1369 C;Superfamily: Aquifex aeolicus hypothetical protein aq_1369	Db 640 VQLKPNKISGLKSHDHHILMQQLDFIALRKVVPRTPLIKLCTFFR 687  RESULT 9  T34757  probable oligopeptide-binding lipoprotein - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: T34757  R; Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. substited to the EMBL Data Library, August 1998
<pre>Query Match Best Local Similarity 22.9%; Pred. No. 6.7; Matches 38; Conservative 26; Mismatches 72; Indels 30; Gaps 7;  Qy 71 PEDIPDVVKQSFPGRYTWRNIMNFEDGAVCTVSNDSSIQGNCFIXHVKFSGINFP 126                                      </pre>	A;Accession: T34757 A;Accession: T34757 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Roscule type: DNA A;Roscidues: 1-600 cMUR> A;Cross-references: EMBL:At031184; PIDN:CAA20180.1; GSPDB:GN00070; SCOEDB:SC2A11.11 A;Experimental source: strain A3(2)
QY 127 NGPVMQKKTQGWEPNTERLFARDGMLIGNNFW-ALKLEGGGHYLCE 171  Db 98 ELGIFQSVEEAMGAFLSTALEHGWEEVPKNYVIYHADFVEGGNKLIAAIKTEEGISTYDQ 157  QY 172 FKSTYKAKKPVKMPGYHYVDRKLDVTNHNKD-YTSVEQCEISIARK 216  Db 158 LKLEEMMKKMVRYPRVVVXSSDVLTYIKDIYEDVQSKAYVIARE 201	Superfamily: dipeptide transport protein  Superfamily: dipeptide transport protein  6.4%; Score 82.5; DB 2; Length 600;  Duery Match 54; Conservative 28; Mismatches 73; Indels 97; Gaps  45 KGGPLPPAWDILSPQCOYGSI-PPTKYPEDIPDYVKQSFPGRYTWERIMN-FE
RESULT 8 \$23818 hypothetical protein Tnp2 - garden snapdragon transposable element Taml c;Species: Antirrhinum majus (garden snapdragon) C;Species: Antirrhinum majus (garden snapdragon) C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Sep-1998 C;Accession: \$23818, \$16551 S;Nacken, W.K.F.; Piotrowiak, R.; Saedler, H.; Sommer, H. submitted to the EMBL Data Library, January 1991 A;Reference number: \$23817 A;Reference number: \$23817 A;Reference number: \$23818 A;Rodession: \$23818 A;Accession: \$23818 A;Accession: \$23818 A;Accession: \$23818	QY 96 DGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGFVMCKTGGMEPNTE 105 QY 96 DGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGFVMCKTGGMEPNTE 143  Db 106 FGAAGAETTPDLATDVAKVSEDGKTYTYTLR-DGVTWEDGKPITSKDVKYGIE 157 QY 144 RLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMP
A;Cross_references: EMBL:X57297 R;Nacken, W.K.F.; Piotrowiak, R.; Saedler, H.; Sommer, H. Mol. Gen. Genet. 228, 201-208, 191- A;Title: The transposable element Tam1 from Antirrhinum majus shows structural homology A;Title: The transposable element Tam1 from Antirrhinum majus shows structural homology A;Reference number: S16551; MUID:91360065; PMID:1715971 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocession: S16551 A;Rocess	Oy 219VACRFF 224    :

20; MUID:97426617;	CEEMCYGHGSCINGTKCICDPGYSGPTCKISTKNPDFLKDDFBGQLESDRFLLMSGGKPS
A,Status: nucleic acid sequence not shown; translation not shown A,Molecule type: DNA A,Residues: 1-390 <blat> A,Cross-references: GB:AE000247; GB:U00096; NID:q1787773; PIDN:AAC74570.1; PID:q1787774;</blat>	95SGLNFPPNGP
train K-12, substrain MG1655	QY 130 VM 146  L
case accivating enzyme Se 6.3%; Score 80.5; 19.4%; Pred. No. 19; active	Qy 147 -ARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMPG 186 
10 KVYMSGTYNGHYEEVEGDGKGKPYEGGUTVRLAV-TKGGPLPF 5	RESULT 12 A89944 alanyl-tRNA synthetase [imported] - Staphylococcus aureus (strain N315) C.Species: Staphylococcus aureus
QY 52 AWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFE-DGAVCTVS 103	C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-Mar-2003 C.Accession: A8994 R.Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch R.Kuroda, M.; Ohta, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
Qy 104 NDSSIQGNCFIXHVKFSGLNFPPNGP 129	Lancet 357, 12: account, m.; Ogasamara, m.; mayasmi, m.; miramacsu, m. Lancet 357, 12: 1226-1240, 2011 A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A,Reference number: A89758; MUID:21311952; PMID:11418146
Qy 130 VMQKKTQGWEDN-TERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMPG 186  Db 226 FMSTIFWQWYKNDVGEIFIRQFESFVSRFLGNGHTSCIFQESCKDNLVVESNGDI 280	<u>አ</u>
Qy 187YHYVDRKLDVTNHNK-DYTSVEQCEISIARKPVVA 220 	A;Cross-references: GB:BA000018; PID:g13701416; PIDN:BAB42710.1; GSPDB:GN00149 A;Experimental source: strain N315 C;Genetics: A;Gene: alas C;Superfamily: alanyl-tRNA ligase
RESULT 11 S58870 reelin precursor - mouse	Query Match Best Local Similarity 21.4%; Pred. No. 63; Matches 43; Conservative 25; Mismatches 56; Indels 77; Gaps 10;
C; Species: Mus musculus (nouse mouse) C; Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 21-Jul-2003 C; Accession: S58870; S71844; I49297 R:P'Arcangelo, G:; Miao, G:G:; Chen, S.C.; Soares, H.D.; Morgan, J.I.; Curran, T.	QY 16 TVNGH-YFEVBGDGKGKPYEGBQTVRLAVTKGGPLPFRAMDILSPQCQYGSIPFTKY 70
Nature 3/4, 719-723, 1995 A,Title: A protein related to extracellular matrix proteins deleted in the mouse mutant A;Reference number: 149297; MUID:95231649; PMID:7715726 A;Accession: 958870	Qy 71 PEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIXHVKFSGLNFPPNGFV 130
A,Status: nucleic acid sequence not shown A,Molecule type: mRNA A,Residues: 1-3461 < ARP> A.Cross-references: EMBL:U24703: NID:q902486; PID:q902487	OY 131 MQKKTQGWEPNTERLFARDGMLIGNNFWALKLEGGGHYLCEFKSTYKAKKPVKMPGYHYV 190 Db 168PNTEIFYDR-GEAXGODDPAREWYPGGRN 195
R;D'Arcangelo, G. submitted to the EMBL Data Library, April 1995 A;Reference number: S71844	191 DRKLDVTNHNKDYT 204  1
A;Molecule type: mRNA A;Residues: 1-215, T',217-1905, 'S',1907-3355,'V',3357-3391,'N',3393-3461 <da2> A;Cross-references: EMBL:U24703; NID:g902486; PID:g902487 F;1-27/Domain: signal sequence #status predicted <sig> F;28-3461/Product: reelin #status predicted <mat> F;1769-1795/Domain: EGF homology <egf></egf></mat></sig></da2>	ein HCF136 [imported] - Ar -ear cress)
Query Match 6.3%; Score 80.5; DB 2; Length 3461; Best Local Similarity 19.9%; Pred. No. 2.9e+02; Matches 56; Conservative 25; Mismatches 75; Indels 125; Gaps 12;	<pre>1 18-Aug-zoou #text_cnange 18-Aug-zoou K.V.; Westhoff, P.</pre>
QY 12 YMSGTVNGHYFEVEGEGKGKPYEGEGTVRLAVTKGGPLFFAWDILSPQ 59	COLLYIN IS ESSENCIAL LOI CIRC
Qy 60 CQYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNF 94	A;Molecule type: mxwa A;Residues: 1-403 <meu> A;Cross-references: EMBL:Y15628; PIDN:CAA75723.1</meu>

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2 VIAKQMTYKVYMSGTVNGHYFEVEG---DGKGKPYEGEQTVRLAVTKGGPLPFAWDILSP 58
                                                                                                                                                                                                                                                                                              85 -- RYTWERIMNFEDGAVCTVSNDSS
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A;Accession: JS0791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-898 <SPI>A;Accession: PU0006
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C;Accession: Cold
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UN; Contains: ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b; ubiquinol-cytoc
C; Species Bradyrhizobium japonicum
C; Date: 12-Oct-1989 #sequence_revision 20-Aug-1994 #text_change 03-Jun-2002
C; Accession: B32382; A39715
C; Accession: B32382; A39715
A; Thoeny-Meyer, L; Stax, D.; Hennecke, H.
Cell 57, 683-697, 1989
A; Theire: An unusual gene cluster for the cytochrome bc-1 complex in Bradyrhizobium japon
A; Reference number: A32382; MUID:89249332; PMID:2541921
A; Accession: B32382
A; Molecule type: DNA
A; Residues: 1-687 < THO>
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R;Thoeny-Meyer, L.; James, P.; Hennecke, H.
Proc. Natl. Acad. Sci. US.A. 88 5001-5005, 1991
A;Title: From one gene to two proteins: the biogenesis of cytochromes b and c-1 in Brady A;Reference number: A39715; MUID:91271320; PMID:1647023
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                                                                                                                                                                                                                       18 NCHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQY-GSIPFTKYPED---
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                                                                                          6.1%; Score 79; DB 2; Length 403
23.9%; Pred. No. 26;
tive 25; Mismatches 89; Indels
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ilarity 22.1%; Pred. No. 52;
Conservative 20; Mismatches
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                                                                                                                                                          49; Conservative
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C;Genetics:
A;Gene: HCF136
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A,Note: host Escherichia coli
C;Date: 17-Mar-1987 #sequence_revision 30-Jun-1987 #text_change 11-Jun-1999
C;Accession: J80791; PU0006; A28165; JU0097; A00717
R;Spicer, E.K.; Konigsberg, W.H.
in Bacteriophage T4, Mathews, C.K., Kutter, E.M., Mosig, G., and Berget, P.B., eds., pp. A;Title: Organization and structure of four T4 genes coding for DNA replication proteins
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A;Cross-references: GB:M10160; GB:J02510; GB:X00769; NID:g2947028; PIDN:AAC05397.1; PID: R;Lamm, N.; Wang, Y.; Mathews, C.K.; Rueger, W.
Eur. J. Biochem. 172, 553-563; 1988
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A;Cross-references: GB:M37159; GB:M28192; NID:g215839; PIDN:AAA21706.1; PID:g215840
C;Comment: This enzyme is required for both initiation and maintenance of viral DNA repli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Deoxycytidylate hydroxymethylase gene of bacteriophage T4: nucleotide sequence A;Reference number: JF0071; MUID:88166734; PMID:3350013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-22 <SP2>
R;Spicer, E.K.; Rush, J.; Fung, C.; Reha-Krantz, L.J.; Karam, J.D.; Konigsberg, W.H.
J. Biol. Chem. 263, 7478-7486, 1988
A;Title: Primary structure of T4 DNA polymerase.
A;Reference number: A28165; MUID:88227938; PMID:3286635
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556 ARSYGRGFPWFIFDFFTQYQEQGPDYVSAVLQGFEEKVPEGVTIPEGSYYNKYFPGHAIK 615
                                                                                                                                                                                                                     -IQGNCFIYHVKFSGLN 123
                                                                                                                                                                                                                                                       90 --RIMNFE-----DGAVCTUS-NDSSIQGNCFIY--HVKFSG------LNFPPNGPVM 131
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DNA-directed DNA polymerase (EC 2.7.7.7) - phage T4
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461 DKHQEGIIPKEIAKVFFQRKDWKKKMFAEE-----MNAEAIKKIIMKGAGS--CSTKPEV 513

Db ò QQ

Search completed: August 12, 2004, 06:14:03 Job time : 25.6701 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                    Copyright
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OM protein - protein search, using sw model

August 12, 2004, 06:12:47; Search time 14.4467 Seconds (without alignments) 847.008 Million cell updates/sec Run on:

US-09-890-463-4 1287 Title:

1 SVIAKQMTYKVYMSGTVNGH......KPVVACRFFRVKSRHKYAVA 235 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20

Post-processing: Minimum Match 0% Maximum Match 100% length: 2000000000

Listing first 45 summaries

SwissProt 42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ជួ	aequorea vi	aspergillus	mus musculu	vibrio chol	aquifex aeo	homo sapien	escherichia	mus musculu	staphylococ	staphylococ	arabidopsis	bradyrhizob	bacteriopha	arabidopsis	rattus norv	caenorhabdi	petunia sp.	methanococc	buchnera ap	luenza b	anabaena sp	petunia sp.	caldocellum	escherichia	influenza b	avian infec	parvovirus	schizosacch	petunia sp.	neisseria g	haemophilus	mus musculu	bacillus su
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SUMMARIES	ID	GFP AEQVI	TRPG ASPNG	NCA2 MOUSE	OSTA_VIBCH	YD69 AQUAE	ENAM_HUMAN	YDEM_ECOLI	RELN MOUSE	SYA_STAAM	SYA_STAAW	H136 ARATH	CYBC_BRAJA	DPOL_BPT4	LOXC ARATH	RELN RAT	UN89_CAEEL	CB21_PETSP	Y642_METJA	MLTA BUCAP	RRP2_INBP9	YY46_ANASP	CB24_PETSP	XYNA_CALSA	YGAF_ECOLI	RRP2_INBSI	VGL2_IBVB	COAT_PAVL3	YA14_SCHPO	CB22_PETSP	ANIA_NEIGO	HXA1 HAEIN	MV10_MOUSE	YHCX_BACSU
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SPCP HUMAN CB2B_LYCES CB2E_LYCES YF99_METJA Y4Q7_KHISN YF97_YEAST CB21_SINAL NRD2_RAT NRD2_RAT NRD2_RAT NRD2_RAT UBPC_YEAST GBUS EAST GBUS EAST GBUS EAST
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## ALIGNMENTS

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SEQUENCE FROM N.A.
MEDLINE=97299832; PubMed=9154981;
Reluwendal G.J.A., Mendes O., Wolbert E.J.H., de Boer A.D.;
Relumendal G.J.A., Mendes O., Wolbert E.J.H., de Boer A.D.;
Enhanced expression in tobacco of the gene encoding green fluorescent protein by modification of its codon usage.";
Plant Mol. Biol. 33:989-999(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cody C.W., Prasher D.C., Westler W.M., Prendergast F.G., Ward W.W.; "Chemical structure of the hexapeptide chromophore of the Aequorea green-fluorescent protein."; Biochemistry 32:1212-1218(1993).
                                                                                                         Aequorea victoria (Jellyfish).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
                                                                                                                                                                                                                                                                                                                                                                                             "Aequorea green fluorescent protein. Expression of the gene and fluorescence characteristics of the recombinant protein."; FEBS Lett. 341:277-280(1994).
                                                                                                                                                                                                                                                                         "Primary structure of the Aequorea victoria green-fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Crystal structure of the Aequorea victoria green fluorescent
                                                                                                                                                                                     [1] — SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE=92175527; PubMed=1347277; Prasher D.C., Eckenrode V.K., Ward W.W., Prendergast F.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE-96355665; PubMed-8703075;
Ormoe M., Cubitt A.B., Kallio K., Gross L.A., Tsien R.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98294543; PubMed=9631087;
Yang F., Moss L.G., Phillips G.N. Jr.;
"The molecular structure of green fluorescent protein.";
Nat. Biocechnol. 14:1246-1251(1996).
          Orf Ann. 19104; Q27903; Created)
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Green fluorescent protein.
 238 AA.
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PRT;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=94185810; PubMed=8137953;
Inouye S., Tsuji F.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93192221; PubMed=8448132;
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 STANDARD;
                                                                                                                                                                                                                                                                                                         Gene 111:229-233(1992).
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 GFP AEQVI
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-i. PTM: Contains a coverently attached chromophore, which is composed of modified amino acid residues. The chromophore is formed upon of modified amino acid residues. The chromophore is formed upon cyclization of the residues. Ser-debydrocyry-GP.

-i. PIOTECHNOLOGY: Has become a useful and ubiquitous tool for making chimeric proteins of GFP linked to other proteins where it functions as a fluorescent protein tag. GFP tolerates N-and C-terminal fusion to a broad variety of proteins. It has been expressed in bacteria, yeast, slime mold, plants, Drosophila, zebrafish, and in mammalian cells. As a noninvasive fluorescent marker in living cells, it allows for a wide range of applications where it may function as a mesaure of protein-protein interactions.

-:-DATABASE: NAME=Protein Spotlight;

WWW="http://www.expasy.org/spotlight/articles/sptltll.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its wes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                           MEDINE-99238303; PubMed-10220315;
Bisliger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;
Bisliger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;
Bisliger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;
"Structural and spectral response of green fluorescent protein
Biochemistry 38:5296-5301 (1939).
-!- FUNCTION: Energy-transfer acceptor. Its role is to transduce the bluorescent light by energy transfer. Fluorescess in vivo upon receiving energy from the Ca(2+)-activated photoprotein aequorin. Absorbs light maximally at 395 nm and exhibits a smaller absorbance peak at 470 nm. The fluorescence emission spectrum peaks at 509 nm with a shoulder at 540 nm.
                              X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION
                                                   MEDLINE=98455509; PubMed=9782051; Wachter R.M., Elsliger M.A., Kallio K., Hanson G.T., Remington S.J.; "Structural basis of spectral shifts in the yellow-emission variants Structure 6:1267-1277(1998).
                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: Photocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, M62654; AAA27722.1;
EMBL, M62653; AAA27721.1;
EMBL, L59345; AAA8846.1;
EMBL, X96418; CAA65278.1;
PIR, JS0692; JQ1514.
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28-AUG-02.
10-APR-02.
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1BFP; 07-JUL-97.
1C4F; 14-JUN-00.
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71 PEDIP--DYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.6%; Score 188.5; DB 1; Length 238; 25.2%; Pred. No. 8.4e-10; ive 46; Mismatches 91; Indels 17;
                                                                                                                                                                                                                      5-imidazolinone (Ser-Gly).
2,3-DIDEHYDROTYROSINE.
F -> Y.
T -> S.
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                                                                                         PDB; ZEMO; ZO-AUG-97.
InterPro; IPR009017; GPP_like.
InterPro; IPR000786; Green_fl_protein.
                                                                                                                                                                                                                                                                     PRINTS, PRO1229, GFLUORESCENT.
ProDom; PD013756; Green fl protein;
Luminescence; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 25.2 nes 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1XYS; 10-APR-02.
1YFP; 28-OCT-98.
2EMD; 20-AUG-97.
2EMN; 20-AUG-97.
2EMO; 20-AUG-97.
                                                                                                                                                       Pfam; PF01353; GFP; 1.
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192 PVLLPDNHYLSTQSALSKDPNEKRDH

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 33:231-238 (1985).

-! FUNCTION: TRIFUNCTIONAL BNZYME BEARING THE GLM AMIDOTRANSFERASE (GATASE) DOMAIN OF ANTHRANILATE SYNTHASE, INDOLE-GLYCEROLPHOSPHATE SYNTHASE, AND PHOSPHOREDSYLANTHRANILATE ISOMERASE ACTIVITIES.

-!- CATALYTIC ACTIVITY: N- (5-phospho-beta-D-ribosyl) -anthranilate = 1-(2-carboxyphenylamino)-1-deoxy-D-ribulose 5-phosphate.

-!- CATALYTIC ACTIVITY: 1- (2-carboxyphenylamino)-1-deoxy-D-ribulose 5-phosphate = 1-(indo)-3-Yl)glycerol 3-phosphate + CO(2) + H(2)O.

-!- CATALYTIC ACTIVITY: Chorismate + L-glutamine = anthranilate +
                                                                                             01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anthranilate synthase component II (EC 4.1.3.27) [Includes: Glutamine amidotransferase; Indole-3-glycerol phosphate synthase (EC 4.1.1.48) (IGPS); N-(5'-phosphoribosyl)anthranilate isomerase (EC 5.3.1.24)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=86137391; PubMed=2936650;
Kos A., Kuijvenhoven J., Wernars K., Bos C.J., van den Broek H.W.J.,
Pouwels P.H., van den Hondel C.A.M.J.J.;
"Isolation and characterization of the Aspergillus niger trpC gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pyruvate + L-glutamate.
PATHWAY: Tryptophan biosynthesis; first step.
PATHWAY: Tryptophan biosynthesis; third step.
PATHWAY: Tryptophan biosynthesis; fourth step.
SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88223483; PubMed=2836085;

Kos T., Kuijvenhoven A., Hessing H.G.M., Pouwels P.H.,

van den Hondel C.A.M.J.J.;

"Nucleotide sequence of the Aspergillus niger trpC gene: structural

relationship with analogous genes of other organisms.";

Curr. Genet. 13:137-144(1988).
                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                          770 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR005220; Anth synthII.
InterPro; IPR001317; CP synthGATase.
InterPro; IPR001309; FWN enzyme.
InterPro; IPR001999; GATase_1.
InterPro; IPR001468; IGPS.
InterPro; IPR001240; PRAI.
InterPro; IPR001240; PRAI.
Fam; PF00117; GATase; 1.
Pfam; PF00117; GATase; 1.
Pfam; PF00118; IGPS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-69 AND 392-433 FROM N.A.
                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, X07071, CAA30107.1, -.
EMBL, M14403, AAA32710.1, -.
EMBL, M14404, AAA32709.1, -.
PIR, S00643; S00643.
HSSP, Q06129, 1QDL.
                                        STANDARD;
                                                  P05328;
01-NOV-1988 (Rel. 09,
"MOV-1988 (Rel. 09,
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           Aspergillus niger
                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5061;
                                        TRPG ASPNG
                                                                                                                                                                                                                                                                                                                                                                  STRAIN=401
                                                                                                                                                                                                     (PRAI)].
                TRPG_ASPNG
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKL---EGGGHYLCEFKSTYK 177
                                                                                                                                                                                                                                                                                                                                       68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P13554; 061950;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Neural cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120)
(NCAM-120).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille M., "Differential exon usage involving an unusual splicing mechanism generates at least eight types of NCAM cDNA in mouse brain."; EMBO J. 8:385-392[1989].
                                                                                                                                                                                                                                                                                                                                       10 KVYMSGTV-NGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFT
                                                                                                                                                                                                                                                                                                                                                                                                     69 KYPE-----DIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barthels D., Santoni M.-J., Wille W., Ruppert C., Caix J.-C.,
Hirsch M.-R., Fontecilla-Camps J.-C., Goridis C.,
"Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
a Mr 79,000 polypeptide without a membrane-spanning region.";
EMBO J. 6:907-914(1987).
                                                                                                                                                                                                                                                                                                       72; Gaps
                            Probom; PD001511; IGPS; 1.
TIGREAMS; TIGR00566; trpG papA; 1.
TIGROSIE; PS00442; GATASE TYPE_1; 1.
PROSITE; PS00614; IGPS; I.
TYPCTOPAn biosynthesis; Isomerase; Lyase; Multifunctional enzyme; Decarboxylase; Transferase; Glutamine amidotransferase.
                                                                                                            Transferase; Glutamine amidotransferase.
219 GLUTAMINE AMIDOTRANSFERASE.
519 INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                         N- (5'-PHOSPHORIBOSYL) ANTHRANILATE
                                                                                                                                                                                                                                                                        6.7%; Score 86; DB 1; Length 770;
24.3%; Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                          61; Indels
                                                                                                                                                                                       104 GATASE (BY SIMILARITY).
199 GATASE (BY SIMILARITY).
201 GATASE (BY SIMILARITY).
82909 MW; 36D8DE5B23097012 CRC64;
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SEQUENCE OF 642-725 FROM N.A.
MEDLINE=88283628; PubWed=3396534;
Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               725 AA
                                                                                                                                                                                                                                                                                                       23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 AKKPVKMPGYHYVDRKLDVTNHNKDY 203
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                                                                                                                                                                            ISOMERASE
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MEDLINE=87246524; PubMed=3595563;
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MEDLINE=89251563; PubMed=2721486;
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                                                                                                                                                                                                                                                                                        24.3%;
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PRINTS; PR00099; CPSGATASE.
PRINTS; PR00096; GATASE.
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201 2
770 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEURAL CELL ADHESION MOLECULE 1, 120 kDa
                                               MEDLINE-86140120; PubMed=3512556;
Rougon G., Marshak D.R.;
"Structural and immunological characterization of the amino-terminal
                                                                                                                    neurites, etc.
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
ALTERNATIVE PRODUCTS:
                                                                                                 ij
"Differential splicing and alternative polyadenylation generates distinct NCAM transcripts and proteins in the mouse."; EMBO J. 7:625-632(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                           domain of mammalian neural cell adhesion molecules."; J. Biol. Chem. 26:3396-3401(1986).
-!- FUNCTION: This protein is a cell adhesion molecule involved neuron-neuron adhesion, neurite fasciculation, outgrowth of
                                                                                                                                                                                                                  SIMILARITY: Contains 5 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG LIKE; 5.
Cell adhesion; Glycoprotein; Repeat; Alternative splicing;
Immunoglobulin domain; Signal; Heparin-binding; GPI-anchor;
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HEPARIN-BINDING (POTENTIAL).
PROBABLE.
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
FIRRONECTIN TYPE-II 1.
FIRRONECTIN TYPE-III 2.
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                                                                                                                                                 Event=Alternative splicing; Named isoforms=3;
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(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC.
                                                                                                                                                                    IsoId=P13594-1; Sequence=Displayed;
                                                                                                                                                                                                Name=N-CAM 140;
Isold=P13595-2; Sequence=External;
                                                                                                                                                                                      IsoId=Pl3595-1; Sequence=External;
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N-LINKED
N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR008957; FN III-like.
InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-like.
InterPro; IPR003588; Ig-c2.
Pfam; PR00041; fn3; 2.
Fam; PR00047; ig; 5.
SMART; SM0060; FN3; 2.
                                                                                                                                                                                                                                                                                                                          EMBL; Y00051; CAA68263.1; -.
EMBL; X15049; CAA33148.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                  X07195; CAA30173.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
                                                                                                                                                                                                                                                                                                                                                                     PDB; 2NCM; 12-MAR-97.
PDB; 3NCM; 23-JUL-99.
MGD; MGI:97281; NCaml.
                                                                                                                                                           Name=N-CAM 120;
                                                                                                                                                                                                                                                                                                                                                            IJMSNG
                                                                                                                                                                             Name=N-CAM 180;
                                       SEQUENCE OF 20-36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3D-structure.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                            PIR; A29673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                   EMBL;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 ----QCQY-----GSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 QGNCFI-----YHVKFSGLNFPPNGPVMQ---KKTQG----WEPNTERLFARDGMLI 153
                                                                                                                                                                                                                                                                                                                                                                                                                          29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20406833; PubMed=10952301;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Determines N-hexane tolerance. Involved in outer membrane permeability. Essential for envelope biogenesis. Could be part of a targeting/usher system for outer membrane components (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455 KIY--NTPSASYLEVTPDSENDFGNYNCTAVNRIGQESLEFILVQADTPSSPSIDRVEPY
                                                                                                                                                                                                                                                                                                                                                                                                                          10 KVYMSGTVNGHYFEVEGDGKGK--PYE-----GEQTVR-LAVTKGGPLPFAWDILSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 GNNFMALKLEGGG----HYLCEFKSTYKAKKP-VKMP-GYHYVDRKLDVTNHNKDY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           619 KVNL--IKODDGGSPIRHYLVKYRALASEWKPEIRLPSGSHHV--MLKSLDWNAEY 670
                                                                                                                                                                                                                                                                                                                                                                            Gaps
N-LINKED (GLCNAC. .) (POTENTIAL).
R-LINKED (GLCNAC. .) (POTENTIAL).
ERSSSVS -> DEKHIFSD (IN REF. 2).
V -> L (IN REF. 2).
OD -> KT (IN REF. 2).
T -> K (IN REF. 2).
T -> K (IN REF. 2).
T -> K (IN REF. 2).
D -> V (IN REF. 2).
P-> V (IN REF. 2).
P-> V (IN REF. 2).
PEL -> REP (IN REF. 2).
PEL -> REP (IN REF. 2).
PEL -> REP (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                          Score 84; DB 1; Length 725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Outer membrane (By similarity). SIMILARITY: Belongs to the imp/ostA family.
                                                                                                                                                                                                                                                                                                                                                                          38; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     513 SSTAQVQFDEPEATGGVPILKYKAEWKSLGEESW--HFTWYD----
                                                                                                                                                                                                                                                                            C2AEB8B4461C6B2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Last sequence update) Crganic solvent tolerance protein precursor. IMP OR OSTA OR VC0446.
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                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                              80296 MW;
                                                                                                                                                                                                                                                                                                                          6.5%;
                                                                                                                                                                                                                                                                                                                                                                          54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 406:477-483(2000).
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2243
3355
3459
572
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603
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657
725 AA;
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          450
479
261
273
354
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572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OSTA VIBCH
Q9KUR9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPOCQYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 VKFSGLNFPPNGPVMQKKTQGWEPNTERLFA------RDGMLIGNNFMAL----- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388 QLSYNYYAPETMKYLDLDLVSHVSRFETDARGKP----SATRVHIEPGLKIPPSNTWGNW 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 QMTYKVYMSGTVN-----GHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFA--WDIL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---AGIVLERDTVLLDDYTQTLEPKIQYLYVPEKYQDNIGLYDSTLLQTDYYGLFRSRKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 TTEAR---VLGTYYQQDLDKTTD------AKLEESVTRVIPEIRSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deckert G., Warren P.V., Gasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V., "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGVDRIESANQVSYGASTRFFDSNYKERINIAFGQIFYLDSKLNPSNKNPDSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 ----KLEGG-----GHYLCEFKSTYKAKKPVKMPGYHYVDRKLDVTNHNKDYTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANIC SOLVENT TOLERANCE PROTEIN: 036718F1896E0F7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 6.5%; Score 84; DB 1; Length 787; Similarity 18.8%; Pred. No. 8.4; 44; Conservative 34; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBL_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       il protein; Complete proteome.
260 AA; 30206 MW; B5D3FB6F37C89BB3 CRC64;
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AQ_1369.
                                                                                                                                                                                                                                                      HANAP; WC: 11.

InterPro; IPR005653; OstA.

InterPro; IPR007643; OstA.

Ffam; PF04958; OstA; 1.

Outer membrane; Signal; Complete proteome.

SIGNAL

1 28
entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000737; AAC07356.1; -.
                                                                                                                                       EMBL; AE004131; AAF93619.1; -.
PIR; E82323; E82323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 787 C
787 AA; 89017 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 392:353-358(1998).
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Hypothetical proteir
SEQUENCE 260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                        TIGR; VC0446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
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                                                                          71 PEDIPDYVKQSFPGRY----TWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPP 126
                                                                                                                                                                                98 ELGIFQSVEEAMGAFLSTALEHGWEEVPKNYVIYHADFVEGGNKLIAAIKTEEGISTYDQ 157
                                                                                                                                                 ----GWE--PNTERLFARDGMLIGNNFM-ALKLEGGGHYLCE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  during
                                                                                               46 PENVREFLIKENYPEKYKLIENWESLQGEFD-----VQKLGGNEYLVIYRIPEKEFEK
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"Enamelin maps to human chromosome 4q21 within the autosomal dominant amelogenesis imperfecta locus.";

Bur. J. Oral Sci. 108:353-358(2000).

-!- FUNCTION: Involved in the mineralization and structural organization of enamel. Involved in the extension of enamel during the secretory stage of dental enamel formation.

-!- SUBCELLULAR LOCATION: Secreted, extracellular matrix.

-!- TISSUE SPECIFICITY: Expressed in tooth particularly in odontoblast, ameloblast and cementoblast.
                                          30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL). (POTENTIAL). (POTENTIAL).
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GO:0030345; F:structural constituent of tooth enamel; NAS.
GO:0030382; P:bone mineralization; NAS.
GO; GO:004776; P:codontogenesis; NAS.
Biomineralization; Extracellular matrix; Glycoprotein; Signal.
                                                                                                                                                                                                                      172 FKSTYKAKKPVKMPGYHYVDRKLDVTNHNKD-YTSVEQCEISIARK 216
                                                                                                                                                                                                                                                       158 LKLEEMMKKMVRYP--RVVVYSSDVLTYIKDIYPDVQSKAYVIARE 201
       DB 1; Length 260;
                                        72; Indels
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16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
   ; Score 83; DB 1
; Pred. No. 2.8;
26; Mismatches
                                                                                                                                                                                                                                                                                                                                               PRT; 1142 AA
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MEDLINE=20489450; PubMed=11037750;
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EMBL; AF210247; AAF73847.1; -.
Genew; HGNC:3344; ENAM.
MIM; 606585; -.
   6.4%;
Query Match 6.4*
Best Local Similarity 22.9*
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                               STANDARD;
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265
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                                                                                                                                                                                                                                                                            72
                                                                                                                                                                                                                                                   18 NGHYFEVEGDGKGKPYEGEQTVRLAVTKG-----GPLPFAWDILSPQCQYGSIPFTKYPE
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97251357; PubMed=9097039; Aiba H., Babba T., Fujita K., Hayashi K., Inada T., Isono K., Aiba H., Rasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;

A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";

DNA Res. 3:363-377(1996).
                       (GLCNAC, .,) (POTENTIAL).
(GLCNAC, .,) (POTENTIAL).
(GLCNAC, .,) (POTENTIAL).
(GLCNAC, .,) (POTENTIAL).
  (POTENTIAL)
                                                                                                                                                       6.3%; Score 81; DB 1; Length 1142; 29.5%; Pred. No. 24;
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                                                                                                                                                                                                      35; Indels
                                                                                                           1142 AA; 128745 MW; 77419C4375EAD6EC CRC64;
(GLCNAC. . .)
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InterPro, IPR007197; Radical SAM.
Pfam, PF04055; Radical SAM; 1.
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551 EIPSPAKEHFPAGRNTWD 568
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EMBL; D90792; BAA15171.1; -.
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                                                                                                                                              Gaps
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Ohashi T., Kusakabe M., Murakami Y., Muramatsu M., Watanabe S.,
Nakao K., Katsuki M., Hayashizaki Y.;
"The reeler gene encodes a protein with an EGF-like motif expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6J; TISSUE-Testis;
MEDLINE-2108-560; Pubmed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Curran T.;
A protein related to extracellular matrix proteins deleted in the mouse mutant reeler.";
Nature 374:719-723(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D'Arcangelo G., Miao G.G., Chen S.-C., Soares H.D., Morgan J.I.,
Curran T.;
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                                                                                 Length 385;
                                                                                                                                           Indels
Hypothetical protein; Complete proteome.
SEQUENCE 385 AA; 44518 MW; 964E34F73E680329 CRC64;
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                                                                                                                                              46; Mismatches 103;
                                                                                    DB 1;
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28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Reelin precursor (EC 3.4.21.-) (Reeler protein)
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                                                                                       Score 80.5;
                                                                                                                  Pred. No.
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MEDLINE=95375789; PubMed=7647795;
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MEDLINE=95231649; PubMed=7715726;
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                                                                                                                                                 54; Conservative
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ALTERNATIVE PRODUCTS:

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MEDLINE=20359755; PubMed=10880573; Exp. Neurol. 156:229-238(1999). BINDING TO VLDLR AND APOER2. Neuron 24:481-489(1999). Cooper J.A., Herz J.; phosphorylation." development." 'Functional FUNCTION Curran 

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ashburner M., Batalov S., Casavant T., Relischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Sızuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., A Hayashizaki Y., 'Bvolutionarily conserved, alternative splicing of reelin during brain "Reelin is a secreted glycoprotein recognized by the CR-50 monoclonal antibody."; annotation of a full-length mouse cDNA collection."; D'Arcangelo G., Nakajima K., Miyata T., Ogawa M., Mikoshiba K., Lambert de Rouvroit C., Bernier B., Royaux I., de Bergeyck V., Goffinet A.M.; Quattrocchi C.C., Wannenes F., Persico A.M., Ciafre S.A., D'Arcangelo G., Farace M.G., Keller F.; "Reelin is a sertine procease of the extracellular matrix."; J. Biol. Chem. 277:303-309(2002). MEDLINE=97325946; PubMed=9182958; Schiffmann S.N., Bernier B., Goffinet A.M.; "Reelin mRNA expression during mouse brain development."; ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY. MEDLINE=99263436; PubMed=10328932; Eur. J. Neurosci. 9:1055-1071 (1997). MEDLINE=21634904; PubMed=11689558; MEDLINE=97141547; PubMed=8987733; Neurosci. 17:23-31(1997). Nature 409:685-690(2001). FISSUE SPECIFICITY. CHARACTERIZATION. CHARACTERIZATION.

SMART; SM00181; EGF; 5.
PROSITE; PS00022; EGF 1; 7.
PROSITE; PS01086; EGF 2; 6.
PROSITE; PS50026; EGF 3; 5.
Hydrolase; Serine proclease; Developmental protein; Matrix protein; Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal; Alternative splicing. SIGNAL 1 2 CHAIN 27 346 Yip J.W., Yip Y.P.L., Nakajima K., Capriotti C.;

"Reelin controls position of autonomic neurons in the spinal cord.";

"Reelin controls position of autonomic neurons in the spinal cord.";

Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616 (2000).

"In layering of neurons in the cerebral cortex and cerebellum.

Regulates microtubule function in neurons and neuronal migration.

Affects migration of sympathetic preganglionic neurons in the spinal cord, where it seems to act as a barrier to neuronal migration. Enzymatic activity is important for the modulation of call adhesion. Binding to the extracellular domains of lipoprotein receptors VLDIR and ApoER2 induces tyrosine phosphorylation of Dabl and modulation of Tau phosphorylation.

"C. -!- SUBCELLULAR LOCATION: Secreted." "Direct binding of Reelin to VLDL receptor and ApoE receptor 2 induces tyrosine phosphorylation of disabled-1 and modulates tau MEDLINE=20036019; PubMed=10571241; Hiesberger T., Trommsdorff M., Howell B.W., Goffinet A.M., Mumby M.C.,

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Name=4 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). Event=Alternative splicing; Named isoforms=3; EMBL; AKO17094; BAR30502.1; A.1.

EMBL; AKO17094; BAR30502.1; A.1.

MGD; MGI.103022; Reln.

GO; GO:0005615; C:extracellular space; IDA.

GO; GO:0007420; P:brain development; IMP.

GO; GO:0016477; P:cell migration; IMP.

InterPro; IPR00280; GGF Ike.

InterPro; IPR00280; Reeler.

Ffam; PF02012; BNR; 15.

Pfam; PF02012; BNR; 15.

Pfam; PF02014; Reeler: 1. -!- SIMILARITY: Belongs to the reelin family. -!- SIMILARITY: Contains 8 EGF-like domains. -!- SIMILARITY: Contains 15 BNR repeats. IsoId=Q60841-2; Sequence=VSP_005577; IsoId=Q60841-1; Sequence=Displayed; EMBL; U24703; AAB91599.1; -. EMBL; D63520; BAA09788.1; ALT_INIT. laminated regions. Name=2; 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -------EDGAVCTVSNDSSIQGNCFIXHVKF-----SGLNFPPNGP 129
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-!- CATALNTIC ACTIVITY: ATP + L-alanine + LENA(Ala) = AMP +
diphosphate + L-alanyl-LENA(Ala).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                             Gaps
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS).
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STRAIN=MISO, ARCC 700699, and N315;
KURDAINE=21311952; PubMed=11418146;
KURDAINE=21311952; PubMed=11418146;
KUROda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Uchiyama I., Baba T., Itian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanahisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba 'Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                        75; Indels 125;
                                                                                                                                                                                                                                                               DB 1; Length 3461;
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NCBI_TaxID=158878, 158879;
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commercial
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                         (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 TVNGH-YFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIP----FTKY 70
                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01411; tRNA-synt 2c; 1.
PRINTS; PR00800; TRNASYNTHALA.
TIGRFAMS; TIGR00344; alas; 1.
PROSITE; PS50860; AA TRNA LIGASE II ALA; 1.
Aminoacyl-tRNA synthetase; Protein Diosynthesis; Ligase; ATP-binding;
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
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10-OCT-2003 (Rel. 42, Last annotation update)
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS)
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Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi J.
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramateu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 876 AA; 98538 MW; 2B2BC79041AC264F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    876 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2%; Score 79.5; I
                                                         or send an email to license@isb-sib.ch).
                                                                                                                                          EMBL, AP003134; BAB42710.1; -.
PIR, A89944; HAMAP; MF.00036; -.
InterPro; IPR003156; DHHAL.
InterPro; IPR002318; tRNA-synt_2c.
InterPro; IPR062318; tRNA-synt_2c.
InterPro; IPR06193; tRNA-synt_Ala.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 DRKLDV-----TNHNKDYT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERYLEVWNLVFSEFNHNKDHS 216
                                                                                                                EMBL; AP003362; BAB57780.1; -. EMBL; AP003134; BAB42710.1; -.
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                                entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sest Local Similarity 21.4% datches 43; Conservative
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                                                                                                                                                                                                                                                                                                                                    Pfam; PF02272; DHHA1; 1.
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SEQUENCE 876 AA
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OBNW87;
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PEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPV 130
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                                            HAMAP; MF 00036; ...; 1...; InterPro; IRR003186; DHHAI.
InterPro; IRR002318; RNA-synt_2c.
InterPro; IRR006193; RNA-synt_2c.
InterPro; IRR006193; RNA-synt_Ala.
Pfam; PF01411; IRNA-synt_2c; 1...
PRINTS; PR01960; TNANSYNTHAIA.
TIGRFAMS; TIGR00344; ala8; PROSITE; PS50860; AA_TRNA_LIGASE_II_ALA; 1...
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 MQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMPGYHYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CV. Wassilewskija, TISSUE=Leaf;
MEDLINE=98409534; Pubmed=9736608;
Meurer J., Pluecken H., Kowallik K.V., Westhoff P.;
Meulear-encoded protein of prokaryotic origin is essential for the stability of photosystem II in Arabidopsis thaliana.";
EMBO J. 17:5286-5297 (1998).
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thallana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicoryledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.

NCBI_TaxID=3702,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20181125; PubMed=10718197;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structural analysis of Arabidopsis thaliana chromosome 5. II. Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned PI clones.";
                                                                                                                                                                                                                                                                                                            77;
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Photosystem II stability/assembly factor HCF136, chloroplast
                                                                                                                                                                                                                                                                             DB 1; Length 876;
                                                                                                                                                                                                                                                                                                               56; Indels
                                                                                                                                                                                                                                         876 AA; 98505 MW; 5D9D662D8DDAEDFC CRC64;
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                                                                                                                                                                                                                                                                          Similarity 21.4%; Score 79.5; D
Similarity 21.4%; Pred. No. 24;
3; Conservative 25; Mismatches
send an email to license@isb-sib.ch)
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ERYLEVWNLVFSEFNHNKDHS 216
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                                EMBL; AP004827; BAB95433.1; -.
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SEQUENCE 876 AA
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MEDLINE=22954850; PubMed=14593172;

Wanda K. Lim J., Dal-G.M., Chen H., Shinn P., Palm C.J., Cheuk R.F.,

Radian-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Ratlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

Arakawa T., Banho F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Enju A., Goldemith A.D., Gurjal M., Hansen N.F.,

Rapschizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

Rhan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Ramiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

Satou M., Tamse R., Vayaberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 --IPD----YVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPVMQKKTQG----WEPNT-----ERLFARDGMLIG---NNFMALKLEGGGHYLC--- 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73
                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: Essential for photosystem II (PSII) biogenesis; putative protein stability or assembly factor for PSII.
-i-SUBCELDULAR LOCATION: Chloroplast; within the thylakoid lumen but attached to the membrane. Restricted to the stromal lamelae.
-i- TISSUE SPECIFICITY: Expression in green tissue, not roots.
-i- DEVELOPMENTAL STAGE: Accumulates also in dark-grown seedlings.
-i- SIMILARITY: Belongs to the yef48 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 NYRFNSISFKGKEGWIIGKPAILLYTADAGE---NWDRIPLSSQLPGDMVFIKATEDKSA
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Pfam; PF02012; BNR; 4.

IIGREAMs; TIGR01409; TAT_signal_seq; 1.

Chloroplast; Thylakoid; Transit peptide; Photosystem II; Membrane.

Chloroplast; Thylakoid; Transit peptide; Photosystem II; Membrane.

TRANSIT 1 53 CHLOROPLAST (POTENTIAL).

TRANSIT 78 THYLAKOID (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y15628; CAA75723.1; -.
EMBL; AB006708; BAB09829.1; -.
EMBL; AY045691; ARK74049.1; -.
EIR; T51828; T51828
InterPro; IPR002860; GH BNR.
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                                                                                                                                                                                                                                                                                                                                   genome.";
Science 302:842-846(2003)
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2 (HEME B566 AXIAL LIGAND)

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40; Conservative
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                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                    687 AA;
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676 ¥ 676
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                                                                                                                                                                                                                                                                                                                                                                 cytochrome c. COFACTOR: Binds three hemes groups, two non-covalently and one covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or BH or b566) is high-potential and absorbs at about 566. Heme 3 is covalently bound like cytochrome
                                                                                                                                                                                                                            MEDLINE=22484999; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.,
                                                                                                                                                                                                                                                                                   "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis. c1 functions as an electron donor to
                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
                                                                                                                                    Thoeny-Meyer L., Stax D., Hennecke H.;
"An unusual gene cluster for the cytochrome bc1 complex in
Bradyrhizobium japonicum and its requirement for effective root
nodule symbosis ";
Cell 57:683-697(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: The protein may be posttranslationally processed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOCHROME B.
CYTOCHROME C1.
THON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
IRON 1 (HEME B562 AXIAL LIGAND).
                                              Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
 01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cytochrome b/cl. [Includes: Cytochrome b; Cytochrome cl].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytochrome c1 and b. SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytochrome cl and the Rieske protein.
                                                                                                                STRAIN=100RIF15;
MEDLINE=89249332; PubMed=2541921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J03176; AAA26200.1;
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687
96
110
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                     STRAIN-USDA 110;
                                  FBCH OR BLR2486.
                                                                                NCBI_TaxID=375;
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556 ARSYGRGFPWFIFDFFTQYQEQGPDYVSAVLQGFEEKVPEGVTIPEGSYYNKYFPGHAIK 615
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(HEME AXIAL LIGAND) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VIAKOMTYKVYMSGTVNGHYFEVEG---DGKGKPYEGEQTVRLAVTKGGPLPFAWDILSP
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MEDLINE=88227938; PubMed=3286635;
Spicer E.K., Rush J., Fung C., Reha-Krantz L.J., Karam J.D.,
Konigsberg W.H.,
"Primary structure of T4 DNA polymerase. Evolutionary relatedness to
eucaryotic and other procaryotic DNA polymerases.";
J. Biol. Chem. 263:7478-7486(1988).
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MEDLINE=22514363; PubMed=12626685;
Miller B.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
"Bacteriophage T4 genome.";
"Mircbiol. Mol. Biol. Rev. 67:86-156(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                      60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-89042102; PubMed=3054876; MEDLINE-89042102; PubMed=3054816; Andrake M., Guild N., Hau T., Gold L., Tuerk C., Karam J.; Andrake M., Guild N., Hau T., Gold L., Tuerk C., Karam J.; "DNA polymerase of bacteriophage T4 is an autogenous translational
                                                                                                                                                                                                                                                                                                           ANCHORS TO THE MEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriophage T4.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
                                                                                                                                                                                                                                                                                                                                                                           Score 79; DB 1; Length 687;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                    61; Indels
                                                                                                                                                                                                                                                                                                                                      A58048F1CF1EFFBB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 42, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Mismatches
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                                                                          POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                      6.1%; Score 79; 22.1%; Pred. No.
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01-JAN-1988 (Rel. 06, Last sequ
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Conservative
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STRAIN=cv. Columbia;
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898 AA;
                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M10160; AACO5397.1.; -

R EMBL; X00769; CAA25344.1; -

R EMBL; AR158101; AAA221706.1; -

R EMBL; M37159; DAA221706.1; -

R PIR; JS0791; DJEPT4.

R PIR; JS0791; DJEPT4.

R PDB; 1NOZ; 14-OCT-96.

R InterPro; IPR006172; DNA_Dol_B.

R InterPro; IPR006133; DNA_Dol_B.

R InterPro; IPR006133; DNA_Dol_B.

R InterPro; IPR006133; DNA_Dol_B.

R R PRINTS; PR00106; DNA_Dol_B.

R PRINTS; PR00106; DNA_Dol_B.

R PRINTS; PR00106; DNA_Dol_B.

R PRINTS; PR00106; DNA_Dol_B.

R PRINTS; PR00106; DNA_Dol_B.

R PRINTS; PR00106; DNA_Dol_B.

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R PRINTS; PR00106; DNA_Dol_B.

R PRINTS; PR00106; DNA_Dol_B.

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R PROSTTE; PR00106; DNA_Dol_B.

R PROSTTE; PR00106; DNA_Dol_B.

R PROSTTE; PR00106; DNA_DOL_B.

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                                                                                                                                                                Biochemistry 35:8110-8119(1996).

-!- FUNCTION: This polymerase possesses two enzymatic activities: DNA synthesis (polymerase) and an exonucleolytic activity that synthesis single stranded DNA in the 3' to 5' direction.

-!- CAȚALYȚIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                     X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1-388.
MEDLINE=96292335; Pubmed=8679562;
Wang J., Yu P., Lin T.C., Konigsberg W.H., Steitz T.A.;
"Crystal structures of an NH2-terminal fragment of T4 DNA polymerase and its complexes with single-stranded DNA and with divalent metal
         MEDLINE=88166734; PubMed=3350013;
Lamm N., Wang Y., Mathews C.K., Rueger W.;
"Deoxycytidylate hydroxymethylase gene of bacteriophage T4.
Nucleotide sequence determination and over-expression of the gene.";
                                                                                                                                                                                                                                  + {DNA}(N).
SIMILARITY: Belongs to the DNA polymerase type-B family.
                                                                                                                                                                                                                                                            DATABASE: NAME=Worthington enzyme manual, WWW="http://www.worthington-biochem.com/DNAPT4/".
                                                                Biochem. 172:553-563(1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --RIMNFE----DGAVCTVS-NDSSIQGNCFIY--HVKFSG------LNFPPNGPVM
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                                                                                                                                                                                                                                                                                                                                                                                                41 LAVTKGGPLPFAWDILSPQCQYGSIPFTKYPED---IP---DYVKQSFPGRYTWE----
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10-OCT-1994 (Rel. 30, Last sequence update)
115-MAR-2004 (Rel. 31, Last annotation update)
115-MAR-2004 (Rel. 31, Last annotation update)
115-MAR-2004 (Rel. 33, Last annotation update)
115-MAR-2004 (Rel. 31, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
                                                                                                                                                                                                                                                                                68;
                                                                                                                                           Length 898;
                                                                                                                                                                                                                                                                         66; Indels
103609 MW; 925300C4CA5C7A24 CRC64;
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27;
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                                                                                                                                    6.1%; Score 79; 22.3%; Pred. No.
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Bell E., Mullet J.E.;
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EMBL; AL138649; CAB72152.1; ALT_SEQ.

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           Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

A Wincker P., Cattolico L., Weissenboch J., Saurin W., Quetier F.,

A Wincker P., Cattolico L., Weissenboch J., Saurin W., Quetier F.,

RA Wincker P., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,

RA Wincker M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,

RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

Ra Conrad A., Hornischer K., Kauer G., Loennert T.-H., Nordsiek G.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,

RA Morarto P., Collado C., Perez-Perez A., Ottenwaelder B., Mewes H.-W.,

RA Morarto P., Collado C., Perez-Perez A., Ottenwaelder B., Mewes H.-W.,

RA Mannhaupt G., Haase D., Schoef H., Rudd S., Zaccaria P., Mewes H.-W.,

RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

RA Rooney T., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,

RA Fraser C.M., Kaneko T., Nakamura Y., Salzberg S.L., White O., Venter J.C.,

RA Fraser C.M., Kaneko T., Nakamura Y., Salzberg S.L., White O., Venter J.C.,

RA Fraser C.M., Kaneko T., Nakamura Y., Salzberg S.L., White O., Wan Aken S.,

RA Kryokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,

RA Saguence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. Columbia;

X MEDLINE=22954850; PubMed=14593172;

MEDLINE=22954850; PubMed=14593172;

A Southwick A.M., Tim J. Dale J.M., Chen H., Shinn P., Palm C.J.,

Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,

A Rarlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,

A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao M., Choy N., Spiu A., Goldsmith A.D., Gurjal M., Hansen N.F.,

Hayashizaki Y., Johnson-Hopson C., Jiang P.K., Jones T., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.K., Jones T., Karnes M.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

Satou M., Tamse R., Vayaberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 302:842-846(2003).

-!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND DEVELOPMENT, PEST RESIZTANCE, AND SENESCENCE OR RESPONSES TO WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING A CIS, CIS-1,4-PENYADIENE STRUCTURE.

-!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-hydroperoxyoctadeca-9,11-diaenoate.

-!- COFACTOR: Iron, one atom tightly bound per molecule (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
SUBCELUIAR LOCATION: Chloroplast (Potential).
TISSUB SPECIFICITY: In leaves and inflorescences but not abundant in seeds, roots and stems.
INDUCTION: By methyl jasmonate and wounding.
SIMILARITY: Belongs to the lipoxygenase family.
SIMILARITY: Contains 1 PLAT domain.
CAUTION: Ref. 2 sequence differs from that shown due to erroneous gene model prediction.
Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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or send an email to license@isb-sib.ch).

EMBL; L23968; AAA32749.1; -

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59 QCQYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              705 WSEVRNIGHG---DKKDEPWWP----VLKTQDDLIGVVTTIAWVTSGHHAAVNFGQYGYG 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    758 GYFPNRPTTTRIRMPTEDPTDEALKEFYESPEKVLLKTYPSQKQATLVMVTLDLLSTHSP 817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   617 YALELSSAVYGKLWRFDQEGLPADLIKRGLAEEDKTAEHGVRLTIP---DYPFAND----
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                    PRINTS, FORTONORT, LIPOXYGENASE.
SMART; SM00308; LH2; 1.
SMOSITE; PS00711; LIPOXYGENASE 1; 1.
PROSITE; PS00001; LAZE, 1.
PROSITE; PS00095; PLATY; 1.
Oxidoreductase; Dioxygenase; Iron; Multigene family; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                           87;
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                                                                                                                                                                                                                                                                                                                                                                                                           97; Indels
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                 F32822205C8F9F22 CRC64;
                                                                                                                                                                                                                                        CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                          IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
W -> C (IN REF. 3).
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CTT-2003 (Rel. 42, Last annotation update)
Reelin precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 30;
31; Mismatches
                                                                                                                                                                                                                                                      LI POXYGENASE.
                                                                                                                                                                                                                                                                                                                                                                                6.1%; Score 78.5;
                       PIR, JQ2391; JQ2391.
HSSP; P08170; 28BL.
SWISS-2DPAGE; P38418; ARATH.
InterPro; IPR000907; Lipoxygenase.
InterPro; IPR001024; Lipoxygenase_LH2.
InterPro; IPR08376; PLAT_LH2.
Pfam; PF00305; Jlpoxygenase; 1.
Pfam; PF01477; PLAT; 1.
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TISSUE=Cerebellum;
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              AY062611; AAL32689.1;
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Best Local Similarity 21.0%
Matches 57; Conservative
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896 AA;
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Kikkawa S., Terash
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MEDLINE=22557166; PubMed=12670697;

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2194 RKCGILSSGNNLFFNEDGLRMLVTRDLDLS-----HARFVQFFMRLGCGKGVPDFRSQP 2247
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3462 AA; 387525 MW; FCCF89B090E035F6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                     Isoid=PS8751-3; Sequence=VSP 005580;
TISSUB SPRCIFICITY: Abundantly produced during brain ontogenesis by the Cajal-Retzius cells and other pioneer neurons located in the telencephalic marginal zone and by granule cells of the external granular layer of the cerebellum.

DOMAIN: The basic C-terminal region is essential for secretion (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characterized by tremor, gait attaxia, cerebellar hypoplasia and abnormal neuronal migration (particularly in the cerebral cortex and hippocampus). The mutation is due to a nucleotide insertion at codon 1892 which results in a translational frameshift and truncation of the protein.

SIMILARITY: Contains 8 EgF-like domains.

SIMILARITY: Contains 15 BNR repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB049473; BAD78470.1; -

R EMBL; AB062600; BAC75467.1; -

R InterPro; IPR002801; GGF like.

R InterPro; IPR002801; EGF.

R InterPro; IPR002801; Reeler.

R Eam; PP02012; BNR; 15.

R Fam; PP02012; BNR; 15.

R FAM; PS02012; BR; 6.

R ROSITE; PS00022; EGF.1; 7.

R ROSITE; PS00022; EGF.1; 7.

R ROSITE; PS00022; EGF.2; 6.

R ROSITE; PS00022; EGF.3; 6.

R ROSITE; PS00022; EGF.3; 7.

R ROSITE; PS00022; EGF.1; 7.

R ROSITE; PS00022; EGF.1; 7.

R ROSITE; PS00022; EGF.1; 7.

R ROSITE; PS00022; EGF.1; 7.

R ROSITE; PS00022; EGF.3; 5.

R ROSITE; PS00025; EGF.3; 5.

R ROSITE; PS00025; EGF.3; 5.

R ROSITE; PS00025; EGF.3; 5.
                                                                                                                                            "Evolutionarily conserved, alternative splicing of reelin during brain
     Yokoi N., Namae M., Wang H.-W., Kojima K., Fuse M., Yasuda K., Serikawa T., Seino S., Komeda K.; Wat neurological disease creeping is caused by a mutation in the reelin gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
DISEASE: Defects in Reln are the cause of creeping, which is
                                                                                                    MEDLINE=99263436; PubMed=10328932;
Lambert de Rouvroit C., Bernier B., Royaux I., de Bergeyck V.,
                                                                                                                                                                                                                                                                                                                                     SUBCELLULÂR LOCATION: Secreted (By similarity) ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P58751-2; Sequence=VSP_005579;
                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P58751-1; Sequence=Displayed;
                                                             Brain Res. Mol. Brain Res. 112:1-7(2003)
                                                                                        ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                         similarity)
                                                                                                                              Goffinet A.M.;
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Name=1;

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---SGLNFPPNGP 129

75; Indels 125; Gaps

---OKKTQGWEPNTERLF--- 146

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Search completed: August 12, 2004, 06:20:09 Job time: 15.4467 secs

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August 12, 2004, 06:19:43 ; Search time 494.559 Seconds (without alignments) 149.169 Million cell updates/sec
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1 SVIAKQMTYKVYMSGTVNGH.......KPVVACRFFRVKSRHKYAVA 235
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 7, Appli	Sequence 8. Appli	Seguence 6, Appli	Seguence 20. Appl	Sequence 4. Appli	Sequence 2. Appli	Segmence 4. Appli	Segmence 67. Appl	Sequence 12. Appl	Sequence 12, Appl	Sequence 12. Appl	Sequence 4. Appli	Sequence 12. Appl	Sequence 8. Appli	Semience 1 Appli
SUMMARIES	ID	US-10-442-148A-7	US-10-442-148A-8	US-10-315-920-6	US-10-121-258-20				US-09-999-745-67				US-10-132-067-4	US-10-006-922-12	US-10-081-864-8	US-10-121-258-1
* Query	th DB	25 15	15	14	14	14	16	16	225 9	10	10	10	12	13	14	14
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Result	No.	п	73	Э	4	2	9	7	80	σ	10	11	12	13	14	15

Seguence 2, Appli		32	13	N	7	1,	7	52,		76,	41	10,	24	9	44	12	4,	Sequence 12, Appl	18,	40,	2	64,	11,	ω	16	Sequence 61, Appl	46	9	Sequence 4, Appli
4 US-10-315-920-2	5 US-10-370-570-56	US-10-406-618	US-10-433	US-10	US-10-739-	US-10	- 1	4 US-10-214-932-52	US-10-343-		6 US-10-423-688A-41	US-1	ns	4 US-10-121-258-6	3 US-10-006-922-44	4 US-10-081-864-12	US-10-121-258	-SD		US-10-161-		5 US-10-370-570-64	US-1	CS	US-10-724-1	US-10-370-5	ns	-10-133-9	10-006
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## ALIGNMENTS

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Sequence 7, Application US/10442148A
Publication No. US20040014242A1
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: HIROTA, KIYONORI
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ORIENTATION-CONTROLLED PROTEIN AND
TITLE OF INVENTION: PROCESS FOR ARRAYING AND IMMOBILIZING PROTEIN USING THE SAME
FILE REPERBUCE: 04583 0103-0000
CURRENT FILING DATE: 2003-05-21
PRIOR APPLICATION NUMBER: UP 2002-148950
FRIOR APPLICATION NUMBER: UP 2002-148950
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein sequence US-10-442-148A-7
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                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 63.0%
Matches 145; Conservative
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ORGANISM: Artificial Sequence
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                                                                                                                                                                              Sequence 8, Application US/10442148A

Publication No. US20040014242A1

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: HARCHA, MISABHIRO

TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ORIENTATION-CONTROLLED PROTEIN AND

TITLE OF INVENTION: PROCESS FOR ARRAYING AND IMMOBILIZING PROTEIN USING THE SAME

TITLE OF INVENTION: PROCESS FOR ARRAYING AND IMMOBILIZING PROTEIN USING THE SAME

TITLE OF INVENTION: PROCESS FOR ARRAYING AND IMMOBILIZING PROTEIN USING THE SAME

TITLE OF INVENTION: DATE: 2003-05-21

CURRENT PRILICATION NUMBER: UP 2002-148950

PRIOR FILING DATE: 2002-05-23

NUMBER OF SEQ ID NOS: 12

SEQ ID NOS: 12

SEQ ID NOS: 12

SEQ ID NOS: 12
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    126 GVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGETHKALKLKDGGHYLVEFKSIYMAKK 185
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                                                181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVACRFFRVKSRH 230
                                                                                     ---RTEGRH 221
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Publication No. US20030175809A1;
GENERAL INFORMATION:
APPLICANT: Fradkov, Arcady Fedorovich
APPLICANT: Fradkov, Arcady Fedorovich
APPLICANT: Fradkov, Alexey
ITILE OF INVENTION: FILORESCENT TIMER PROTEINS AND METHODS
ITILE OF INVENTION: FOR THEIR USE
FILE REFERENCE: CLON-077CIP
CURRENT APPLICATION NUMBER: 05/211,607
PRIOR FILING DATE: 2002-12-09
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 239;
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63.0%; Pred. No. 4.7e-76;
tive 27; Mismatches 44;
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ORGANISM: Artificial Sequence
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Best Local Similarity 63.0°
Matches 145; Conservative
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US-10-442-148A-8
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US-10-315-920-6
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121 GLNFPPNGPVMQXXTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
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APPLICANT: Campbell, Robert
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
FILE REFERENCE: UC083.1CP2CP1
CURRENT APPLICATION NUMBER: 09/10/121,258
CURRENT PAPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 225
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                                                                                                Length 225;
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; FEATURE:
; OTHER INFORMATION: variant of sequence from Discosoma
US-10-315-920-6
                                                                                                                                                       44;
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63.0%; Pred. No. 1.2e-75;
tive 27; Mismatches 44;
                                                                                                Query Match
61.0%; Score 785; DB 14;
Best Local Similarity 63.0%; Pred. No. 9.1e-76;
Matches 145; Conservative 27; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 PVOLPGYYYVDSKLDITSHNEDYTIVEQYE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: DsRed with I125R US-10-121-258-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/10121258; Publication No. US20030059835A1; GENERAL INFORMATION:
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Matches 145; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFWALKLEGGGHYLCEFKSTYKAKK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC 60
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| Publication No. US20040110225A1
| GENERAL INFORMATION:
| APPLICANT: Glabs, Parrick D.L.
| APPLICANT: Carter, Robert W. |
| APPLICANT: Schmale, Michael C. |
| TILLE OF INVENTION: ELUORESCENT PROTEINS FROM AQUATIC SPECIES
| FILE REFERENCE: 638.004
| CURRENT FILING DATE: 2002-12-09
| NUMBER OF SEQ ID NOS: 15
| SEQ ID NO 2
| LENGTH: 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVACRFFRVKSRH 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
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                                                      APPLICANT: Fradkow, Arcady Fedorovich
APPLICANT: Fradkow, Arcady Fedorovich
APPLICANT: Terskikh, Alexey
TITLE OF INVENTION: FLUCRESCENT TIMER PROTEINS AND METHODS
TITLE OF INVENTION: FOR THEIR USE
FILE REFERENCE: CLON-077CIP
CURRENT APPLICATION NUMBER: US/10/315,920
CURRENT APPLICATION NUMBER: 60/211,607
PRIOR APPLICATION NUMBER: 60/211,607
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: RESERED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 60.9%; Score 784; DB 14; Length 225; Best Local Similarity 63.0%; Pred. No. 1.2e-75; Matches 145; Conservative 27; Mismatches 44; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: variant of sequence from Discosoma sp. US-10-315-920-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: mutant red fluorescent protein US-10-314-936-2
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  ; Sequence 4, Application US/10315920; Publication No. US20030175809A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 63.0%
Matches 145; Conservative
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ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                          SEQ ID NO 4
LENGTH: 225
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                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                      6 NVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILSPQF 65
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SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
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Patent No. USZO020157120A1
GENERAL INFORMATION:
APPLICANT: THE RECENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGER Y.
APPLICANT: TSIEN, GGOEFREY
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: REGEN1470-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/316,920
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Publication No. US20040110225A1
GENERAL INFORMATION:
APPLICANT: Gibbs, Patrick D.L.
APPLICANT: Schmale, Michael C.
TITLE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPECIES
FILE REFERENCE: 638 1004
CURRENT APPLICATION NUMBER: US/10/314,936
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ 1D NOS: 15
SOFTWARE: Patentin version 3.1
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Best Local Similarity
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LENGTH: 225
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LENGTH: 22!
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Sequence 12 Application US/09866538

publication Wo. US20030032088A1

GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: TSIEN, ROGER

APPLICANT: Campbell. Robert

TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS

FILE REFERENCE: REGENIS30-2

CURRENT APPLICATION NUMBER: US/09/866,538

CURRENT APPLICATION NUMBER: US/09/866,538

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin version 3.0

SEQ ID NO 12

LENGTH: 225
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                                                                                                                                                                                               60.8%; Score 783; DB 9; Length 225;
llarity 63.0%; Pred. No. 1.5e-75;
Conservative 27; Mismatches 44; Indels
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                    NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.0
PRIOR FILING DATE: 1999-05-21
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/ ORGANISM: Discosoma sp.
US-09-866-538-12
                                                                                                                             ORGANISM: Discosoma sp
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Best Local Similarity
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Best Local Similarity
Matches 145; Conserv
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                                                              SEQ ID NO 67
LENGTH: 22
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                                                                                                           TYPE: PRT
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RESULT 10 US-09-794-308-12

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Publication No. US20030186229A1
GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGER
APPLICANT: THIG, Alice
APPLICANT: THIG, Alice
APPLICANT: THIG, Alice
APPLICANT: THOS, Alice
APPLICANT: THOS, Alice
APPLICANT: TO INVENTION: EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
TITLE OF INVENTION: EMISSION RATIOMETRIC INDICATORS OF CURRENT APPLICATION UNMBER: US/09/865,291
CURRENT PILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 12
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Sequence 12, Application US/09794308

Publication No. US20030170911A1

GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, Roger
APPLICANT: ACHARIAS, David
APPLICANT: BAIRD, Geoffrey
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: REGENTS:0
CURRENT PILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 25
NUMBER: Patentin version 3.0
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63.0%; Pred. No. 1.5e-75;
tive 27; Mismatches 44;
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Best Local Similarity 63.0%
Matches 145; Conservative
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us-09-890-463-4.rapb

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Sequence 8, Application US/10081864
Publication No. US20030022287A1
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                                                                                                                                                                                                                                                                                Local Similarity
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                  QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
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APPLICANT: Lunyarov, Arcady F.
APPLICANT: Labas, Yulii A.
APPLICANT: Labas, Yulii A.
APPLICANT: Labas, Yulii A.
APPLICANT: Matz, Mikhail V.
APPLICANT: Terskikh, Alexey
TITLE OF INVENTION: No. US20020197676Alel Chromophores/Fluorophores and
TITLE OF INVENTION: Methods for Using the Same
TITLE OF INVENTION: Methods for Using the Same
CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/120,330
PRIOR FILING DATE: 1999-12-11
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR FILING DATE: 1999-12-09
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                                                                               44; Indels 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: red fluorescent protein (dsRED) US-10-132-067-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.8%; Score 783; DB 12;
63.0%; Pred. No. 1.5e-75;
tive 27; Mismatches 44;
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Publication No. US20020197676A1
GENERAL INFORMATION:
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Best Local Similarity 63.0%
Matches 145; Conservative
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APPLICANT: Lukyanov, Sergey
APPLICANT: Lukyanov, Konstantin
APPLICANT: Lukyanov, Konstantin
APPLICANT: Sauchevich, Yuriy
APPLICANT: Savistky, Alexandr
APPLICANT: Fradkov, Arcady
TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
TITLE OF INVENTION: Methods for Using the Same
TITLE REFERENCE: CLON-667
CURRENT FILING DATE: 2002-06-19
FRIOR PILING DATE: 2001-12-04
FRIOR FILING DATE: 2001-12-04
FRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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------RTEGRH 221
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60.8%; Score 783; DB 14; Length 225;
Best Local Similarity 63.0%; Pred. No. 1.5e-75;
Matches 145; Conservative 27; Mismatches 44; Indels 1
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PRIOR APPLICATION NUMBER: 09/458,144
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-19
NUMBER: OF FELING DATE: 1999-11-19
NUMBER: OF FELING DATE: 1999-11-19
SEQ ID NO 12
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61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
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                                                                                   1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVŢKGGPLPFAWDILSPQC 60
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Best Local Similarity 63.0%; Pred. No. 1.5e-75;
Matches 145; Conservative 27; Mismatches 44; Indels 14; Gaps
                                                                                                                                                                                                                                               RESULT 15

US-10-121-258-1

US-10-121-258-1

Publication No. US20030059835A1

GENERAL INFORMATION:

APPLICANT: Taien, Roger

TITLE OF INVENTION: PROTEIN VARIANTS AND DIMERIC FLUORESCENT

TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME

TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME

TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME

CURRENT APPLICATION NUMBER: US/10/112,258

CURRENT APPLICATION NUMBER: 09/794,308

PRIOR FILING DATE: 2002-04-10

PRIOR FILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 78

SOGTWARE: FASELED FOR WINDOWS VERSION 4.0

SEQ ID NO 1

LENGTH: 225
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                                                                                                                                                181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVACRFFRVKSRH 230
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                                                                                                                                                                      completed: August 12, 2004, 06:51:22 ne : 495.559 secs
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// DCATION: (1)...(225)

OTHER INFORMATION: wild-type DsRed

US-10-121-258-1
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1287
1 SVIAKQMTYKVYMSGTVNGH.....KPVVACRFFRVKSRHKXAVA 235
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                  OM protein - protein search, using sw model
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RESULT 1 HS-09-277-716	1.7-716-	ا بر					
; Sequence	nce 16,	Applica	tion	60/	US/09277716A		
; Patent	t No. 6	$\sim$ c					
, APPL:	APPLICANT:	Bryan, B					
; APPL	APPLICANT:			Chr	Christopher		
	OF II	OF INVENTION:	LUCIFERASES	RAS	SES, FLUORESCENT PROTEINS,	NUCLEIC ACIDS	ENCODING
CURRENT		APPLICATION N FILING DATE:	NUMBER: US/		US/09/277,716A		
		APPLICATION NUMBER:	NUMBER	· .	60/102,939		
		FILING DATE: 1998-10	: 1998-	10-			
; EAKLIEK		APPLICATION NUMBER: 60/089 FILING DATE: 1998-06-15	NUMBER	פיים	50/089,367 15		
; EARLIER		APPLICATION NUMBER	NUMBER	9	60/079,624		
; EARLIER	- (	FILING DATE: 1998	1998-	-03-	-27		
, SOFT	' 띭	Patentin '	Ver. 2.	0			
SEQ II	ID NO 16	<u>د</u>					
TYPE	. K	200					
, ORG		Renilla r	mulleri				
; FEA.	FEATURE: OTHER INFC	FEATURE: OTHER INFORMATION:	Renilla		mulleri Green Fluorescent	ant Protein (GFP)	
US-09-277	77-716-	-16					
Query Best ] Match	Query Match Best Local S Matches 96	imi ;	37 44 vativ	.3%; .0%;	; Score 479.5; DB 3; ; Pred. No. 8.8e-45; 41; Mismatches 74;	Length 238; Indels 7; Gaps	3;
δy	7	MTYKVYMS	GTVNGHY	FEV	MTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLFFAWDILSPQCQYGSIP		99
Db	15	:    : MSYKVNLE	 GIVNNHV	FT.	:   ;		74
ò	67		PDYVKOS	FPG	FTKYPEDI PDYVKOSFPGRYTWERIMNFEDGAVCTVSNDSSIOGNCFIYHVKFSGLNFPP		126
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186 GYHYVDRKLDVTNHNKDYTSVEQCEISIAR-----KPV 218 

RESULT 2 US-09-609-161B-16

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RESULT 5
US-09-626-580C-65
is Sequence 65, Application US/09626580C
is Patent No. 6562617
is GENERAL INFORMATION:
is APPLICANT: Bogenberger, Jakob M.
is APPLICANT: Peele, Beau R.
is APPLICANT: Peele, Beau R.
is APPLICANT: Peele, Beau R.
is APPLICANT: Peele, Beau R.
is APPLICANT: Peele, Beau R.
is APPLICANT: Peele, Beau R.
                                                                                                                                                                                                                                                                                                                                    135 DGPVMQKTILGIEPSFEAMYMNNGVLVGEVILVYKLNSGKYYSCHMKTLMKSKGVVKEFP 194
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Fatent No. 6548632

GENERAL INFORMATION:

APPLICANT: Anderson, David

TITLE OF INVENTION: Fuelons of Scaffold Proteins with Random Peptide

TITLE OF INVENTION: Libraries

TITLE OF INVENTION: 1.69900-1/RMS/AMS

CURRENT FILING DATE: 1999-10-08

CURRENT FILING DATE: 1999-10-08

FRIOR FILING DATE: 1999-10-08

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 65

LENGTH: 238
                                                                                                                               15 MSYKVNLEGIVNNHVFTWEGCGKGNILFGNQLVQIRVTKGAPLPFAFDIVSPAFQYGNRT
                                                                                                  7 MTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIP
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Length 238;
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37.3%; Score 479.5; DB 4; 44.0%; Pred. No. 8.8e-45;
                                               41; Mismatches
                       Best Local Similarity 44.0%
Matches 96; Conservative
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US-09-415-765B-65
  Query Match
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                                  APPLICANT: Brand Bruce
APPLICANT: Brand Bruce
APPLICANT: Brand Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
TITLE REFERENCE: 24729-1218
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/102,939
PRIOR APPLICATION NUMBER: 60/102,939
PRIOR PLING DATE: 1998-06-15
PRIOR PLING DATE: 1998-06-15
PRIOR PLING DATE: 1998-06-15
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
SOUTHARRE: PATENTIN VET: 2.0
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Patent No. 6548249
GENERAL INFORMATION:
APPLICANT: Anderson, David
TITLE OF INVENTION: Libraries
FILE REPRENDANCE: A-66900-3/RMS
CURRENT APPLICATION NUMBER: US/09/626,581D
CURRENT PILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/169,015
PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Renilla mulleri Green Fluorescent Protein (GFP) US-09-609-161B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 37.3%; Score 479.5; DB 4; Length 238; Best Local Similarity 44.0%; Pred. No. 8.8e-45; Matches 96; Conservative 41; Mismatches 74; Indels 7.
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SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUCITITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USB THEREOF IN DIAGNOSTICS, HIGH TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-1218
CURRENT APPLICATION WUMBER: 105/09/609,161B
PRIOR APPLICATION UNMER: 09/277,716
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Patent No. 645761
GENERAL INFORMATION:
APPLICANT: Stratagene
TITLE OF INVENTION: Humanized Polynucleotide Sequence Encoding Renilla Mulleri Green
Patent No. 6645761
TITLE OF INVENTION: Fluorescent Protein
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                                                  127 NGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGGHYLCEFKSTYKAKKPVK-MP 185
                                                                           67 FTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPP 126
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195 EYHFIHHRLEKT-YVEEGSFVEQHETAIAQLTTIGKPL 231
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44.0%; Pred. No. 8.7e-44;
live 42; Mismatches 73
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PRIOR PEDLICATION NUMBER: 60/102,939
PRIOR FILING DATE: 1998-10-01
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1998-06-15
NUMBER OF SEQ ID NOS: 32
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APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
                                                                                                                                                                                                                                                                                    Sequence 32, Application US/09609161B Patent No. 6436682 GENERAL INFORMATION:
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SEQ ID NO 32
LENGTH: 238
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Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               74; Indels
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APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT
CURRENT APPLICATION NUMBER: US/09/277,716A
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/102,939
EARLIER FILING DATE: 1998-10-01
EARLIER FILING DATE: 1998-10-01
EARLIER PELING DATE: 1998-06-15
EARLIER PELING DATE: 1998-06-15
EARLIER FILING DATE: 1998-03-27
NUMBER: OF SEQ ID NOS: 32
FILE REFERENCE: A-66900-2/RMS/AMS
CURRENT APPLICATION WUMBER: US/09/626,580C
FURENT FILING DATE: 2000-07-27
FRIOR APPLICATION NUMBER: US 09/415,765
FRIOR FILING DATE: 1999-10-08
FRIOR FILING DATE: 1999-10-08
FRIOR FILING DATE: 1999-10-08
NUMBER: OF SEQ ID NOS: 65
SEQ ID NO 65
                                                                                                                                                                                                                                                                                                                                                                               41; Mismatches
                                                                                                                                                                                                                                                                                                                                    37.3%; Score 479.5; 44.0%; Pred. No. 8.8
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ORGANISM: Renilla muelleri
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LENGTH: 238
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APPLICANT FORDS. Krista

TITLE OF INVENTION: Mutants of Green Fluorescent Protein
FILE REFERENCE: 0942, 4020002

CURRENT APPLICATION NUMBER: US 09/970, 762

PRIOR APPLICATION NUMBER: US 09/970, 762

PRIOR FILING DATE: 1999-11-14

PROR APPLICATION NUMBER: US 60/030,935

PRIOR FILING DATE: 1996-11-15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 17

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l Similarity 25.7%; Pred. No. 9.2e-14;
53; Conservative 46; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Mismatches
FILE REFERENCE: 25436/1755
CURRENT APPLICATION NUMBER: US/09/839,650
UNRENT FILING DATE: 2001-04-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
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; ORGANISM: Aequorea victoria, Al mutant
US-09-472-065A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.4%;
43.6%;
                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Renilla muelleri
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95; Conservative
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LENGTH; 238
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Best Local 8
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71 PEDIP--DYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :: | : : |: :: |: :: |135 NILGHKLE-YNYNSHNVYIMADKQKNGIKV--NFKIIRHIEDGSVQLADHYQQNTPIGDG 191
                                                                       APPLICANT: FRAZEK, IA Hector
APPLICANT: FRAZEK, IA Hector
APPLICANT: ZHOU, Jian
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AND METHOD FOR SELECTIVELY
TITLE OF INVENTION: EXPRESSING A PROTEIN IN A TARGET CELL OR TISSUE
FILE REFERENCE: 210318.0001/1US
CURRENT APPLICATION NUMBER: US/09/479,645A
CURRENT FILING DATE: 2000-01-07
PRIOR FILING DATE: 1998-0-0-07
PRIOR FILING DATE: 1998-0-0-09
PRIOR FILING DATE: 1998-0-0-09
PRIOR FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 219
SEQ ID NOS: 219
SEQ ID NO 12
LENTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 VELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTT-GKLPVPWPTLVTTFSYGVQCFSRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 VYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic gfp OTHER INFORMATION: gene (Papillomavirusized)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.0%; Score 193.5; DB 4; Length 238; 25.2%; Pred. No. 3.3e-13; Live 47; Mismatches 90; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Codons of humanized gfp gene replaced with OTHER INFORMATION: synonymous codons used at relatively high OTHER INFORMATION: frequency by papillomavirus genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 PVKMPGYHYVDRKLDVT---NHNKDY 203
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ADDRESSEE: MORGAN & FINNEGAN
; Sequence 12, Application US/09479645A; Patent No. 6489141; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 25.28
Matches 52; Conservative
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71 PEDIP--DYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 VELDGDVNGHKRSVSGEGEGDATYGKLTLKRICTT-GKLPVPWPTLVTTFSYGVQCFSRY 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91:
                                                                                                                                                                                                                                    REGISTRATION NUMBER: 33,285
REFERENCE/DOCKET NUMBER: 2955-4004US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.8%; Score 190.5; DB 26.2%; Pred. No. 7e-13;
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TITLE OF INVENTION: HYBRID MOLECULES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,946B
FILING DATE: 13-Feb-1998
PRIOR APPLICATION DATA:
                 APPLICATION NUMBER: US/09/023,946B
FILING DATE: 13-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,805
FILING DATE: 14 FEBRUARY 1997
APPLICATION NUMBER: 60/038,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: UNKNOWN SEQUENCE DESCRIPTION: SEQ ID NO: 23:
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                                                                                                                                                                                                           NAME: KENNETH H.SONNENFELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36, Application US/09023946B Patent No. 6670449 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: FLOPPY DISK
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                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
  CURRENT APPLICATION DATA:
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ADDRESSEE: MORGAN &
                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 54; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVMQKKTQGWEPNTERLF----ARDGMLIGNNF-MALKLEGGGHYLCEF--KSTYKAKK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: | :: | :: | :: | :: | 135 NILGHKLE-YNYNDHQVYIMADKQKNGIKV--NPKIRHNIEDGGGVQLADHYQQNTPIGDG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 VYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFTKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.0%; Score 192.5; DB 4; Length 238; 25.7%; Pred. No. 4.2e-13; tive 46; Mismatches 90; Indels 17
                                                                                                                                                                                                                                                                                                                          NAME: KENNETH H.SONNENFELD
REGISTRATION NUMBER: 33,285
REFERENCE/DOCKET NUMBER: 2955-4004US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/09023946B
Patent No. 6670449
GENERAL INFORMATION:
APPLICANT: GEREO MIESENBOCK, ET AL.
TITLE OF INVENTION: HYBRID MOLECULES AND
                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,946B
FILING DATE: 13-Feb-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 28:
                                                                                                                                                                                                         APPLICATION NUMBER: 60/036,805
FILING DATE: 14 FEBRUARY 1997
APPLICATION NUMBER: 60/038,179
FILING DATE: 13 FEBRUARY 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :| :| :|:
PVLLPDNHYLHTQSALSKDPNEKRDH 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: FLOPPY DISK
                      MEDIUM TYPE: FLOPPY DISK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10154
COMPUTER READABLE FORM:
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COMPUTER READABLE FORM:
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                                                                                          SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 421792
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Matches 53; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-023-946B-23
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 VYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFTKY 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 VELDGDVNGHKKFSVSGEGEGEDATYGKLTLKFICTT-GKLPVPWPTLVTTFSYGVQCFSRY 74
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                                                                                                                                                                                                                                                                                                                                                                Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                  92; Indels
                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                          14.7%; Score 189.5; DB 4
25.9%; Pred. No. 9.1e-13;
ive 45; Mismatches 92
                                                                   NAME: KENNETH H.SONNENFELD
REGISTRATION NUMBER: 33,285
REFERENCE/DOCKET NUMBER: 2955-4004US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/09023946B
Patent No. 6670449
GENERAL INFORMATION:
APPLICANT: GERO MIESENBOCK, ET AL.
TITLE OF INVENTION: HYBRID MOLECULES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,946B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 36:
FILING DATE: 14 FEBRUARY 1997
APPLICATION WUMBER: 60/038,179
FILING DATE: 13 FEBRUARY 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 13-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14 FEBRUARY 1997
APPLICATION NUMBER: 60/038,179
FILING DATE: 13 FEBRUARY 1997
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VLLPDNHYLHTQSALSKDPNEKRDH 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: KENNETH H.SONNENFELD
                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                    STRANDEDNESS: UNKNOWN TOPOLOGY: UNKNOWN
                                                                                                                                                                         TELEX: 421792
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                     TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                53; Conservative
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ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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US-09-023-946B-22
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71 PEDIP--DYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 PEDIP--DYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :: | :: | :: | :: | 135 NILGHKLE-YNYNDHQVYIMADKQKNG--IKANFKIRHNIEDGGVQLADHYQQNTPIGDG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 VELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTT-GKLPVPWPTLVTTFSYGVQCFSRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 VYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFTKY
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                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                 4; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.7%; Score 189; DB 4; Length 94 ilarity 22.1%; Pred. No. 7.4e-12; Conservative 52; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 172, Application US/09513783A

Patent No. 6416959
GENBEAL INFORMATION:
APPLICANT: Giuliano, Kenneth A.
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT PILING DATE: 2000-02-25
CURRENT FILING DATE: 2000-02-25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 172
                    REFERENCE/DOCKET NUMBER: 2955-4004US2
TELECHOMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFRAK: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                         14.7%; Score 189; DB 4, ilarity 27.4%; Pred. No. 1e-12; Conservative 39; Mismatches 8
                                                                                                                                                                                                            TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
SEQUENCE DESCRIPTION: SEQ ID NO:
REGISTRATION NUMBER: 33,285
                                                                                                                 TELEX: 421792
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity
Trahes 52; Conserva
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Best Local Similarity
Matches 62; Conserv
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US-09-513-783A-172
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181 PVKMPGYHYVDRKLDVTNHNKDYTSVE 207	193 PVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYKSGMSVVGIDLGFQ 252	208 QCEISIARKPVVACRFFRVKSRHKYAVA 235	253 SCYVAVARAGGIETIANEYSDRCTPACISFGPKNRSIGAAA 293	
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Search completed: August 12, 2004, 06:21:07 Job time : 25.5594 secs

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OM protein - protein search, using sw model

Run on:

August 12, 2004, 06:34:08; Search time 16 Seconds (without alignments) 30.060 Million cell updates/sec

US-09-890-463-1 21 1 SVIAK 5 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

206 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		carbon-monoxide de	hypothetical prote	$\vdash$	phosphoprotein, bo		hypothetical prote		qlycoden phosphory	hypothetical prote		T-cell receptor be	T-cell receptor be	rotami	P1 -	ribosomal protein	ribosomal protein	ribosomal protein	hypothetical prote		u	thyroglobulin - do	22K superhelical D	T-cell_receptor be		l monooxya	cocoonase (EC 3.4.	abt		chain
SUMMARIES	1	PL0146	I40505	A27897	S11127	S17255	T30569	E44823	A60521	T14908	161883	PT0551	PT0697	137013	w	(7)	I39966	I39965	T14910	S55237	PT0597	S18401	A61300	PT0534	PT0721	A44955	B61168	I50385	PT0278	PT0295
DB		ď	7	7	7	~	7	7	N	7	7	7	~	7	~	7	7	7	7	N	7	~	7	C)	~	7	7	7	7	7
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Result No.		<del>~</del>	N	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

seminal plasma pro	34.5K structural p	35K structural pro	growth-modulating	bursin - chicken	histidinol dehydro	bradykinin-potenti	bradýkinin-potenti	T-cell receptor be	phagocytosis-stimu	phenol 2-monooxvge	phospholipase C (E	endoglucanase F -	hypothetical prote		myosin-light-chain
S62883	B44817	D44817	GKHU	A60898	S13894	E37196	F37196	PT0578	A02147	A37832	I40870	I40804	T46627	JQ1273	839390
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6 28.6	6 28.6	6 28.6	5 23.8	5 23.8	5 23.8	5 23.8	5 23.8	5 23.8	5 23.8	5 23.8	5 23.8	5 23.8	5 23.8	5 23.8	5 23.8
3.0	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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Appothetical protein 3 (4 aa) - Bacillus stearothermophilus
C.Species: Bacillus stearothermophilus
C.Species: Bacillus stearothermophilus
C.Species: Bacillus stearothermophilus
C.Species: Bacillus stearothermophilus
C.Spate: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
C.Accession: I40505
R.Waye, M.M.; Winter, G.
Bur. J. Blochem. 128, 505-510, 1986
A.Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA synth
A.Raccession: 140505
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-4 <RES>
A.Cross-references: EMBL:X04193; NID:g40233; PIDN:CAA27783.1; PID:g580944

Gaps ; 0 Query Match
42.9%; Score 9; DB 2; Length 4;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 3; Mismatches 0; Indels

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RESULT 3 A27897

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C,Accession: T30569
R;Morciscion: T30569
R;Morciscion: T30569
Curr. Genet. 34, 379-385, 1998
A;Title: Isolation and characterisation of the acetyl-CoA carboxylase gene from Aspergil) A;Reference number: Z20869; MUID:99087906; PMID:9871120
A;Accession: T30569
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N.Alternate names: glycogen phosphorylase b
C.Species: Liza ramada
C.Jate: Liza ramada
C.Jate: Liza ramada
C.Jate: Liza ramada
C.Jate: Liza ramada
C.Jate: Liza ramada
C.Jate: Liza ramada
C.Jate: Liza ramada
C.Jate: Liza ramada
C.Jate: Banante, I.V.
R.Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A.Title: Purification and characterization of glycogen phosphorylase B from skeletal mus A.Reference number: A60521; MUID:90227907; PMID:2109669
A.Accession: A60521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Accession: E44823
R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
Neurosci. 11, 3412-3421, 1991
A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is A;Reference number: A44823; MUID:92044785; PMID:1941090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Cross-references: EMBL: Y15996; NID:e1285512; PID:e1218041; PIDN: CAA75927.1
                                                                                                                                                                                                                                                                              hypothetical protein - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synaptosomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)
N;Alternate names: superprotein peptide 1
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
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A;Experimental source: visual tissue
A;Experimental source: visual tissue
A;Note: sequence extracted from NCBI backbone (NCBIP:64247)
C;Keywords: membrane trafficking
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                Pred. No. 2.8e+05;
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Pred. No. 2.8e+05;
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Best Local Similarity
Matches 2; Conserv
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                Best Local Similarity
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S17255
ribosomal protein YmL1, mitochondrial, questionable - yeast (Saccharomyces cerevisiae) (C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
A;Variety: strain 07173
C;Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-May-1997
C;Accession: S17255
R;Grohmann, L.; Graack, H.R.; Kruft, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.FBES Lett. 284, 51-56, 1991
A;Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from A;Reference number: S17255; MUD:91285106; PMID:2060626
A;Accession: S17255
A;Moolecule type: protein
A;Residues: 1-4 cGRO>
C;Comment: A coding region for this protein could not be identified in the genome of Sac C;Genetics:
A;Genoment: A coding region for this protein biosynthesis; ribosome
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - Aspergillus phoenicis (fragment)
NyAlternate names: glucoamylase
C;Species: Aspergillus phoenicis
C;Species: Aspergillus phoenicis
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 06-Dec-1996
C;Accession: A27897
R;Inokuchi, N.; Takahashi, T.; Irie, M.
J. Biochhem. 90, 1055-1067, 1981
A;Title: Purification and characterization of a minor glucoamylase from Aspergillus sait
A;Reference number: A27897; MuID:82075730; PMID:6796572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphoprotein, bone - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 21.Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
C;Accession: S11127; S11128
B;Mikuni-Takagaki, Y.; Glimcher, M.J.
Biochem. U. 268, 585-591, 1990
A;Title: Post-translational processing of chicken bone phosphoproteins. Identification A;Reference number: S11127; MUID:90303246; PMID:2363696
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A, Molecule type: Drotein
A, Residues: 1-4 - INO>
C, Keywords: glycosidase, hydrolase, polysaccharide degradation
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 'X', 2-5 <MIK2>
C,Keywords: phosphoprotein
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A;Molecule type: protein
A;Residues: 1-5 <MIK1>
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Best Local Similarity
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Query Match

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C;Species: Cercopithecus patas
C;Date: 19-7013
R;Queralt, R.;Oliva, R.
Gene 133, 197-204, 1993
A;Title: Identification of conserved potential regulatory sequences of the protamine-enco
        J. Exp. Med. 174, 115-124, 1991
Afrittle: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0551
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J. Exp. Med. 174, 115-124, 1991
A: Exp. Med. 174, 115-124, 1991
A;Title: Juncitional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0697
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0697
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A;Molecule type: DNA
A;Residues: 1-4 <RESA
A;Cross-references: EMBL:Z12150; NID:g22814; PIDN:CAA78134.1; PID:g4377415
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Pred. No. 2.8e+05;
2; Mismatches 0; Indels
                                                                                                       A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-4 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
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Best Local Similarity 33.3%;
Matches 1; Conservative
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Best Local Similarity 50.0°
Matches 1; Conservative
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C:Species: Pongo pygmaeus (orangutan)
C:Species: Pongo pygmaeus (orangutan)
C:Species: Pongo pygmaeus (orangutan)
C:Accession: 161883
R;Queralt, R.; Oliva, R.
Gene 13, 197-204, 1993
A;Title: Identification of conserved potential regulatory sequences of the protamine-end A;Reference number: 137013; MUID:94040810; PMID:8224908
A;Status: If1883
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 <RES>
A;Cross-references: EMBL:Z12146; NID:g38156; PIDN:CAA78130.1; PID:g4379372
                        A;Residues: 1-5 <BON>
C;Superfamily: glucan phosphorylase
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim
                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Date: 20-8ep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T14908
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A;Title: CPRP4a, a novel plant bZIP protein of the CPRF family: comparative analysis of
A;Reference number: Z18261; MUID:98265918; PMID:9604882
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A;Molecule type: mRNA
A;Residues: 15 <KIR>
A;Cross-references: EMBL:Y10809; NID:g3336901; PIDN:CAA71767.1; PID:g3336902
A;Experimental source: Hamburger Schnitt
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C,Species: Mus musculus (house mouse)
C,Bacels: 7-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
R,Feeney, A.J.
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33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indele
                                                                                                                                                        38.1%; Score 8; DB 2; Length 5; 100.0%; Pred. No. 2.8e+05; tive 0; Mismatches 0; Indel.
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A; Molecule type: protein A; Residues: 1-5 <BON>
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C;Species: Papio hamadryas doguera (savannah baboon)
C;Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C;Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C;Accession: Is4439
A;Title: Identification of conserved potential regulatory sequences of the protamine-enc A;Reference number: 137013; MUID:94040810; PMID:8224908
A;Accession: I84439
A;Accession: IS4439
A;Accession: Is4439
A;Accession: Lyelminary; translated from GB/EMBL/DDBJ
A;Accession: Lyelminary; translated from GB/EMBL/DDBJ
A;Accession: Lyelminary; Translated from GB/EMBL/DDBJ
A;Accessiones: L4 cRES>
A;Coss-references: EMBL:Z12147; NID:g38134; PIDN:CAA78131.1; PID:g4379349
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139964
ribosomal protein S4 - Bacillus circulans (fragment)
C; Species: Bacillus circulans
C; Species: Bacillus circulans
C; Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C; Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C; Date: 13964
R; Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A; Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A; Reference number: 139963; MulD:93015735; PMID:1400226
A; Residue: 139964
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-5 <RES>A; Cross-references: GB:M99041; NID:g143471
C; Genetics:
A; Genetics:
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Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels
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Search completed: August 12, 2004, 06:55:20 Job time : 17 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 12, 2004, 06:21:13; Search time 13 Seconds (without alignments) 20.027 Million cell updates/sec

Run on:

US-09-890-463-1 21 1 SVIAK 5 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

38 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	- न	P19918 pseudomonas	515 saccharomy	P38639 mus musculu	homo sa	vibri	P58705 anthopleura		citro			P13973 escherichia	P35904 achatina fu		antho				P41853 artioposthi					litoria	19991	P54714 canis famil	~			_		20	01162	P01373 periplaneta
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P01151 sus scrofa P19916 pseudomonas P13071 citrobacter P58648 octopus min P81864 pardachirus
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4 4 4 0 0 8 8 8 0 0 0
44400
33.4 3.7 3.7 3.7

# ALIGNMENTS

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MS PSECH DCMS_PSECH STANDARD; PRT; P19918; 01-FEB-1991 (Rel. 17, Created) 01-FEB-1991 (Rel. 17, Last sequence 28-FEB-2003 (Rel. 41, Last annotatic Carbon monoxide dehydrogenase small		SEQUENCE.  MEDLINE=90055678; PubMed=2818128;  Kraut Hugendieck I., Herwig S., Meyer O.;  "Homology and distribution of CO dehydrogenase structura carboxydetrophic bacteria.";  Arch. Microbiol. 152:335-341(1989).  -!- FUNCTION: Catalyzes the exidation of carbon monoxide dioxide.	-:- CATALTIC ACTIVITY: CO + H(2/O + acceptor = CO(2/) + reduced acceptor:- COFACTOR: Binds 2 2Fe-2S clusters:- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND SMALL. PIR, PLO146; PLO146. Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S. NON TER 4 4 4 SEQÜENCE 4 AA; 420 MW; 6DD33DD6F000000 CRC64;	Query Match 47.6%; Score 10; DB 1; Length 4; Best Local Similarity 66.7%; Pred. No. 1.40+05; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 3 IAK 5 1	RESULT 2  RM01 YEAST  TD _RM01 YEAST  TO _1-70N-1994 (Rel. 29, Created)  DT 01-70N-1994 (Rel. 29, Last sequence update)  DT 01-70N-1994 (Rel. 29, Last annotation update)  DT 01-70N-1994 (Rel. 29, Last annotation update)  DT 01-70N-1994 (Rel. 29, Last annotation update)  DT 01-70N-1994 (Rel. 29, Last sequence update)  DT 01-70N-1994 (Rel. 29, Last sequence update)  DT 01-70N-1994 (Rel. 29, Last sequence update)  DT 01-70N-1994 (Rel. 29, Last sequence)  DT 01-70N-1994 (Rel. 29, Last sequence)  DT 01-70N-1994 (Rel. 29, Last sequencing of proteins of the large ribosomal RL FEBS Lett. 284:51-56(1991).
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-!- MISCELLANEOUS: This serum tripeptide has been found to stimulate growth of some cell types and to inhibit other types in vitro. GO; GO:0001558; P:regulation of cell growth; NAS. SEQUENCE 3 AA; 340 MM; 6331E81000000000 CRC64;
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IISSUE-Fibroblast;

MEDLINE-9500907; PubMed=7523108;

Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

Merrick B.A., Patterson R.M., Michter L.L., He C., Selkirk J.K.;

Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

Separation and sequencing of familiar and novel murine proteins

using preparative two-dimensional gel electrophoresis.",

Electrophoresis 15:735-745(1994)

-!- MISCELLANBOUS: On the 2D-gel the determined pl of this unknown

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-OCT-1994 (Rel. 30, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i; Indels
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                                                                                4 AA; 402 MW; 7771B2D5D000000 CRC64;
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33.3%; Pred. No. 1.4e+05;
tive 1; Mismatches 1;
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last amnotation update)
Growth-modulating peptide.
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                   SGD; L0002681; MRPL1.
Ribosomal protein; Mitochondrion.
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Best Local Similarity 100.00
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2; Conservative
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DB 1; Length 3;

Score 5;

23.8%;

Query Match

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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A new Vibrio fischeri lux gene precedes a bidirectional termination site for the lux operon.";

Bacteriol. 172.197-6802(1990).

-!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.

IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS STBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.

-!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate + an acyl-protein thiolescer.

-!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
                                                                                                                                                                                                                                                                                                   01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acyl-
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Eukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Actiniaria,
Nynantheae, Actiniidae, Anthopleura.
NCBI_TaxID=6110;
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Vibrionaceae, Vibrio.
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  Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                   3 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                protein synthetase) (Fragment).
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1; Conservative
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ses 1; Conserv
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us-09-890-463-1.closed.rsp

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1; Conservative
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P12997;
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                                                                                                                                 MCFarlane 1.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.,
"The expansion behaviour of sea anemones may be coordinated by two
inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";
Proc. R. Soc. Lond., B. Biol. Sol. 253:18811993).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle
groups. May be involved in the expansion phase of feeding
behaviour in sea anemones.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.; The characteristics, isolation and synthesis of the phagocytosis stimulating peptide tuffsin."; Biochem. Biophys. Res. Commun. 47:172-179(1972).
                Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.; risolation of L.J.-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropeptide from sea anemones."
Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GO; GO:0006909; P:phagocytosis; NAS.
SEQUENCE 4 AA; 501 MW; 74176321C000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               L-3-PHENYLLACTYL.
AMIDATION.
6DD339C9A0000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phagocytosis-stimulating peptide (Tuftsin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AA.
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1; Conservative 0; Mismatches
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WEDLINE=92028852; PubMed=1681803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                       4 AA; 512 MW;
                                                                                                                                                                                                                                                                                                                                                               Neuropeptide; Amidation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                    PIR, JQ1273; JQ1273.
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Best Local Similarity
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDIINE=89006280; PubMed=2971595;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli, citrobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
-!- PATHWAY: Biotin biosynthesis; last step.
-!- SIMILARITY: Belongs to the biotin and lipoic acid synthetases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Last sequence update)
8-FEB-2003 (Rel. 41, Last annotation update)
Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting enzyme inhibitor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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Cintra A.C.O., Vieira C.A., Giglio J.R.;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M21922; -; NOT ANNOTATED CDS.
PIR; 140698; 140698.
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                                                                                                                                                                                                                                              Enterobacteriaceae; Citrobacter
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Matches

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MEDLINE=88227859; PubMed=2836369;
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01-JUN-1994
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ACH1 ACHFU
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structure and biological activity of bradykinin potentiating
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Australian buzzing tree frog
skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Litoria rubella (Desert tree frog).
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid IncFII R100.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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0
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0
                peptides from Bothrops insularis snake venom.",
J. Protein Chem. 9:221-227 (1990).
-1- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.
PIR, G37196, G37196.
Hypotensive agent; Pyrrolidone carboxylic acid.
SEQÜENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;
                                                                                                                                                                                                                                    23.8%; Score 5; DB 1; Length 5; 100.0%; Pred. No. 1.4e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.8%; Score 5; DB 1; Length 5; 50.0%; Pred. No. 1.4e+05; live 1; Mismatches 0; Indels
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5 AA, 616 MW, 61F2D1A059A00000 CRC64;
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01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
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nes 1; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Bukaryota, Metazoa, Mollusca, Gastropoda, Pulmonata, Stylommatophora,
Sigmurethra, Achatinoidea, Achatinidae, Achatina.
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"Purification of achatin-I from the acria of the African giant snail, Achatina fulica, and its possible function.",
Biochem. Biophys. Res. Commun. 177:847-853 (1991).
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Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
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Inamoto S., Yoshioka Y., Ohtsubo B.,
"Identification and characterization of the products from the trady and trary genes of plasmid R100.",
-i. Bacteriol. 170:2749-2757(1988).
-i. FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION PROCESS OF BACTERIAL GELLS FOR THE EXCHANGE OF PLASMID DNA.
-i. SUBCELLULAR LOCATION: Cytoplasmic.
-i. SIMILARITY: Belongs to the tram family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.8%; Score 5; DB 1; Let 100.0%; Pred. No. 1.4e+05; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
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MEDLINE=91264856; PubMed=1675568;
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PIR; A32014; A32014.
Conjugation; Plasmid; DNA-binding.
NON TER
SEQUENCE 5 AA; 634 MW; 6B1B1AA44
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MEDLINE=89273551; PubMed=2597281;
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Best Local Similarity
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-!- MISCELLANBOUS: These peptides are released from mast cells in lung (and other tissues) during hypersensitivity reactions (anaphylaxis). Their activities, preferentially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of enzymes, and stimulation of the hexose monophosphate shunt. GO; GO:0006935; P:chemotaxis, IDA.

GO; GO:0006935; P:chemotaxis, IDA.

VARIANT

| V -> A (IN OTHER PEPTIDE).

| FITId=UAR 005201.
| FITIG=UAR 005201.
-!- FUNCTION: Neuroexcitatory peptide, increases the impulse frequency and produces a spike broadening of the identified heart excitatory neuron (PON); also enhances the amplitude and frequency of the heart heat. Has also an effect on several other muscles.

PIR; A32480; A32480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goetzl B.J., Austen K.F.; "Purification and synthesis of eosinophilotactic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor of
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Antho-Tamide I [Contains: Antho-Rlamide II].
Anthopleura elegantissima (Sea anemone).
Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
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                                                                                                                                          2 2 D-PHENYLALANINE.
4 AA; 408 MW; 6AADD9C810000000 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last amotation update)
Eosinophilotactic peptides.
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                                                                                                                      Hormone; D-amino acid.
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McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
"The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-Kaamide and Antho-Riamide.";
Proc. R. Soc. Lond., B. Biol. Sci. 253:183-188 (1993).
-!-FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.
-!- SUBCELIULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron specific.
Neuropeptide; Amidation.
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                                                           anemones: the unusual,
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-!- FUNCTION: Cardioactive, has both positive chronotropic and
inotropic effects on the heart. Ocp-4 is a 1000 time less
Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D., Grimmelikhuijzen C.J.P.;
"Isolation of two novel neuropeptides from sea anemones: the biologically active L-J-phenyllactyl-Tyr-Arg-Ile-NH2 and its Res-phenyllactyl fragment Tyr-Arg-Ile-NH2.";
Peptides 12:1165-1173(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AA; 598 MW; 60441B59A000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 2 D-SERINE (IN OCP-4).
4 AA; 463 MW; 6AB365BB10000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.0%; Score 4; DB 1; Le: 100.0%; Pred. No. 1.4e+05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTHO-RIAMIDE I.
ANTHO-RIAMIDE II.
L-3-PHENYLLACTYL.
AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
-!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cardioactive peptides Ocp-3/Ocp-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 AA.
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Best Local Similarity
Matches 1; Conserv
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Best Local Similarity
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MOD RES
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Matches
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Search completed: August 12, 2004, 06:53:27 Job time : 14 secs

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

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Rattus sp.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
"ILME: a waterborne pheromonal peptide released by the eggs of Sepia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Mollusca, Cephalopoda, Coleoidea, Neocoleoidea,
Decapodiformes, Sepioidea, Sepiidae, Sepia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zatylny C., Marvin L., Gagnon J., Henry J.;

"Fertilization in Sepia officinalis: the first mollusk sperm-
attracting peptide.";

Biochem. Biophys. Res. Commun. 296:1186-1193(2002).

-!- SUBCELULAR MYOTROPIC ACTIVITY TARGETING THE GENITAL TRACT.

-!- SUBCELULAR LOCATION: FOLLICLE, FULLY GROWN OCCYTE AND EGG(EC2).

-!- TISSUE SPECIFICITY: FOLLICLE, FULLY GROWN OCCYTE AND EGG(EC2).

-!- MASS SPECIFICITY: MW-505.4; METHOD-MALDI.

GO; GO:0005186; F:pheromone activity; IEA.
                                                                                                                                          STRAIN=Gunn;
MEDLINE=91282758; PubMed=1840486;
Sato H., Aono S., Kashiwamata S., Koiwai O.;
"Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat.";
Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
                                                                                                                                                                                                                                                                                                                                DB 11; Length 4;
                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Bilirubin UDP-glucuronosyltransferase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P83568;
01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                          NON TER 1 1 1
SEQUENCE 4 AA, 473 MW; 633732C42000000 CRC64;
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Biochem. Biophys. Res. Commun. 275:217-222(2000)
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Pred. No. 1e+06
2; Mismatches
                                                                                                                                                                                                                                                          GO; GO:0016740; F:transferase activity; IEA
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Sepia officinalis (Common cuttlefish).
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Similarity 33.3%;
1; Conservative ;
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Best Local Similarity
                                                                                                                             SEQUENCE FROM N.A.
                                                                                               NCBI_TaxID=10118;
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PubMed=12207899;
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TISSUE≈Egg;
PubMed=10944467;
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1 NVL 3
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P83073 bacillus ce
Q99007 hordeum vul
P83308 gallus gall
P83570 sepia offic
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                                                                                                         August 12, 2004, 06:32:33 ; Search time 75 Seconds (without alignments) 21.035 Million cell updates/sec
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                                 Compugen Ltd.
                GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compug
                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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P83073
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sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
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sp_vertebrate:*
sp_unclassified:*
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sp_rodent:*
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Match Length
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Score

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RESULT 1

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Gaps

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vallub galine (chicken).
Bukaryora, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                               PubMed=6137771;
Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
"A novel active pentapeptide from chicken brain identified by
antibodies to FMRFamide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Mollusca, Cephalopoda, Coleoidea, Neocoleoidea,
Decapodiformes, Sepioidea, Sepiidae, Sepia.
NCBI_TaxID=6610;
                                                                                                                                                                 NATURE 305:328-330(1983).
-!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
-!- SIMILARITY: BELONGS TO THE FARP (FWRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                   9.5%; Score 2; DB 13; Length 5; 0.0%; Pred. No. 1e+06; tive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                   GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
Neuropeptide; Amidation.
MOD RES 5 5 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION TISSUE-Optic lobe;
                                                                                                                                                                                                                                                                                                                                                                                                                                       P83570;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Neuropeptide GWa.
Sepia officinalis (Common cuttlefish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD RES 2 AMIDATION.
SEQUENCE 2 AA; 261 MW; 73781000000000 CRC64;

        MOD RES
        5
        AMIDATION.

        SEQUENCE
        5 AA; 645 MW; 69D4073767400000 CRC64;

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0; Mismatches
FMRFamide-like neuropeptide (LPLRF-amide) Gallus gallus (Chicken).
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0.0%; E
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les 0; Conservative
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                                                                                          SEQUENCE, AND SYNTHESIS.
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nes 0; Conserv
                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9437704;
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91329704; PubMed=1831055;
MEDLINE-91329704; PubMed=1831055;
Jacobsen J.V., Close T.J.;
"Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature bareley aleurone layers.";
Plant Mol. Biol. 16:713-721 (1991).
EMBL; X54643; CAA38455.1;
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                                                                                   01-007-2001 (TrEMBLrel. 18, Created)
01-007-2001 (TrEMBLrel. 18, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
88 kDa protein (Fragment).
Bacillus cereus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.8%; Score 5; DB 10; Length 5; 50.0%; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                  Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                       5 AA; 623 MW; 6B01AAA336F00000 CRC64;
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                                                                                                                                                                                                                                                                                 23.8%; Score 5; DB 2; L 100.0%; Pred. No. 1e+06; tive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                     STRAIN-NCIMB 11796;
Browne N., Dowds B.C.A.;
Submitted (JUL-2001) to Swiss-Prot.
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                                                                                                                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha amylase (Fragment)
AMY1 GENE.
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                                                               PRELIMINARY;
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US-09-890-463-1 21 Perfect score:

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34717 Total number of hits satisfying chosen parameters:

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geneseqp1980s:* geneseqp1990s:* geneseqp2001s:* geneseqp2011s:* geneseqp2013as:* geneseqp2013as:* A Geneseq 29Jan04:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

SUMMARIES	Descrip	7147 Aay97147 Pigment	ABB99061 Abb99061 N-termina	AAR72928 Yeast PPI	AAR72927 Yeast PPI	AAR72884 Yeast PPI	AA029981 Peptide		AAP97806 Sequence		AAY07986 Human sec	AAP91629 Aap91629 Motif use	AAP97808 Sequence		ABB84333 Human MBP	ABR57300 Thermus	AAR12661 Aar12661 Pentapept	AAR51525 Mimotope	AAR69893 Pentameri	AAR78989 AAR78989 p107 pept	AAR98639 Peptide	AAR15757 Farnesyl	AAR49753 Farnesylt	AAR77816 Farnesyl	AAW04443 Farnesv]	0::5::
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AAY28344 AAY87947 AAG56468 AAB57512 AAB57522 AAB57566 AAG05144 AAB63437 AAB50561 AAB70151	ADD11758 AAF11310 AAR11930 AAR11699 AAR71699 AAR69878
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#### ALIGNMENTS

RESULT 1

N-terminal; pigment protein from coral tissue; PPCT; fluorescence; tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet; UV filter. Pigment protein from coral tissue N-terminal peptide 1. AAY97147 standard; peptide; 5 AA. 02-FEB-2000; 2000WO-AU000056. (first entry) Acropora aspera.
Acropora horrida.
Montipora caliculata.
Montipora monasteriata. Porites murrayensis. Porites lobata. WO200046233-A1. 10-AUG-2000. 04-DEC-2000 AAY97147; AAY97147 ID AAYS 

99AU-00008463 02-FEB-1999;

ŝ Hoegh-Guldberg O, Dove (UNSY ) UNIV SYDNEY

WPI; 2000-532892/48.

Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.

Claim 3; Page 42; 49pp; English.

The N-terminal peptides shown in AAY97147-48 are from pigment protein from coral tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-660 nm and a maximal fluorescence emission is in the range of 330-700 nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to follow gene expression in transformed tissues) or general dysetuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters

(biomatrix). The first all-protein

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situations of distorted light spectra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated colour-facilitating molecule (CFM)

Comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

con-white light or particle emission. CFMs are useful for producing a

transgenic animal which exhibits a novel colour e.g. sheep with blue or

red coloured fleece. They are useful for producing coloured plant

catracts, e.g. flavouring, beverage or juice or colouring agent. Other

uses include transducing or intensifying an image, providing additional

light for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

upholstery. CFMs are useful in the flower inductry, in the development of

new varieties of flowering plants. Other contemplated uses include,

expression markers, general reporter molecules, photon traps, UV sinks or

in sunscreens. CFMs modify visible colour in edible and/or ornamental

fungal species, and in fruits and vegetables to enhance their

marketability. CFMs embedded in a gel matrix improve image quality in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      industry; expression marker; reporter molecule; photon trap;
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                                                                100.0%; Score 21; DB 3; I
100.0%; Pred. No. 1.4e+06;
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Prescott M;
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                                                                                                                                                                                                                                                   ABB99061 standard; peptide; 5 AA
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21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
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(UYQU ) UNIV QUEENSLAND.
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                                   Sequence 5 AA;
 (both claimed)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New E.coli peptidyl prolyl cis trans isomerase beta - used to accelerate the folding of proteins, partic. for activation of inactive recombinant
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chromophore to be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a
                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli, protein conformation, folding, acceleration, PPIase-alpha, peptidyl prolyl cis trans isomerase alpha, catalysis, isomerisation, prolyl peptide bond.
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Pred. No. 1.4e+06;
1; Mismatches 0; Indels
                                                                                                                 0; Indels
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                                                                                    100.0%; Score 21; DB 5; I
100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
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                            colour-facilitating molecule (CFM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 23; 85pp; English.
                                                                                                                                                                                                                                               AAR72928 standard; peptide; 5 AA.
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89JP-00260244.
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75.0%;
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25-MAR-2003
29-NOV-1995
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06-OCT-1989;
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2 VIAK 5

AAR72927

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AAR72877-85 are tryptic fragments of a yeast PPIase (peptidyl prolyl cistrans isomerase). The yeast PPIase has a single mol. wt. of about 17 kba and a single isoelectric point of about 6.2. The enzyme catalyses the isomerisation of prolyl peptide bonds in proteins and accelerates the folding of the protein. The inventors are claiming the PPIase-alpha. (Updated on 25-MAR-2003 to correct PM field.) (Updated on 25-MAR-2003 to correct PM field.) (Updated on 25-MAR-2003 to not 05-MAR-2003 to correct PM field.) (Updated on 15-MAR-2003 to correct PM field.) (Updated on 16-OCT-2003 to standardise 05 field)
                                                                                                                                                                                                                                                                                                                                                                                                                                         New B.coli peptidyl prolyl cis trans isomerase alpha - used to accelerate the folding of proteins, partic. for activation of inactive recombinant proteins.
                                                             Bscherichia coli; protein conformation; folding; acceleration;
PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;
isomerisation; prolyl peptide bond.
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75.0%; Pred. No. 1.4e+06;
tive 1; Mismatches 0;
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                                                                                                                                    Saccharomyces cerevisiae; strain AH22
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                                   Yeast PPlase tryptic fragment 8.
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89JP-00344705.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              94EP-00203612
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(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Katou S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-140756/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TOFU ) TONEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIAK 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5 AA;
|:||
WAK
                                                                                                                                                                    16-OCT-2003
25-MAR-2003
29-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-1990;
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25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-1989;
06-OCT-1989;
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                                                                                                                                                                                                                                                                                                                                                                           EP647714-A1
                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayano T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR72884;
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Indels Length 5;

RESULT 5

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Gaps

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The inventors claim recombinant penicillin acyltransferase (PAT) and DNA coding for PAT. PAT catalyses the last step in the biosynthesis of penicillin G and penicillin V. More specifically, the coding strand of the DNA has the nucleotide sequence shown below. This includes three introns and codes for a PAT protein with mol. wt. ca. 40kD. Plasmid vectors pBC2001 and pBC2002 are specifically claimed
  released). The method is useful in quantifying the actual amount of 1 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of fragment 19, the tryptic fragment of recombinant penicillin acyltransferase (PAT) polypeptide 2.
                  more selected polypeptides in a sample, which may be important in research settings (e.g. in drug discovery and development) and in clinical settings (e.g. for medical diagnosis and for monitoring treatment efficacy). The present sequence is a peptide used to demonstrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant penicillin acyl-transferase - and DNA coding for it.
                                                                                                                                                                         Score 16; DB 7; Length 5;
Pred. No. 1.4e+06;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.4%; Score 15; DB 1; Length 5; 60.0%; Pred. No. 1.4e+06; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weber G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penicillin biosynthesis; enzyme; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palma N,
                                                                                                                                                                                                                                                                                                                                                                                           AAP97806 standard; protein; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88AT-00000922.
88AT-00001806.
88AT-00002201.
                                                                                                                                                                             76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89EP-00106214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leitner E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Conservative
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penicillium chrysogenum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 48; 52pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BIOC ) BIOCHEMIE GMBH
                                                                                                                                                                                             Similarity
3; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1989-294357/41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVIAR
                                                                                                                                                                                                                                                      SVIAK
                                                                                                                                                                                                                                                                                             SWWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5 AA;
                                                                                                                                        Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-APR-1988;
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08-SEP-1988;
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Best Local
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                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                       AAP97806
  8888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·.
                                                                                                                                                                                                                                                  The invention relates to peptides having cell adhesion, growth, expression or secretion-enhancing activities. The peptides of the invention are useful for enhancing cell growth and/or secretion in a cell culture system. The present sequence is a peptide used to enhance cellular adherence and growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determining the actual amount of a polypeptide in a sample by measuring the amount of a cleavage product released from the polypeptide and using an exogenous polypeptide corresponding to the cleavage product as a
                                                                                                                                                        New peptide, useful for enhancing cell growth and/or secretion in a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method of determining the actual amount of 1 or more selected polypeptides in a sample, which comprises releasing specific cleavage products from each of the polypeptides with cleavage agents and determining the actual amount of the product by comparison to a defined amount of a corresponding exogenous polypeptide (the actual amount of each of the cleavage products is directly related to the actual amount of the selected polypeptide from which it was
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                             Haaland PD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quantitation; amount of protein; rat; human;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 5;
                                                                           Wilkins JH,
                                                                                                                                                                                                                                                                                                                                                                                                         76.2%; Score 16; DB 6; I
llarity 75.0%; Pred. No. 1.4e+06;
Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat purinergic receptor P2X3 peptide #2.
                                                                             G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 7; 26pp; English.
                                                                             Spargo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR63446 standard; peptide; 5 AA
                                                                                                                                                                                                                Claim 3; Page 44; 78pp; English.
                                      BECTON DICKINSON & CO.
19-NOV-2001; 2001US-00992124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-NOV-2002; 2002WO-US038334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-2001; 2001US-0334325P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (THER-) THERMO FINNIGAN LLC.
                                                                           Heidaran M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         purinergic receptor; P2X3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lindall AW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
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                                                                                                                  WPI; 2003-482396/45
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Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIAK 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WAK 5
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                                                                                                                                                                           culture system
                                                                                                                                                                                                                                                                                                                                                                       Sequence 5 AA;
                                                                           Campbell RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barnidge DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-2003
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ABR63446

RESULT 7 ABR63446

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Query Match

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σ AAR61324 RESULT

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New de-acetylase specific for L-N-acetyl-phosphinothricin - isolated from soil microbes, useful for stereoselective prodn. of L-phosphinothricin and for making male-sterile plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   deacetylase has a molecular weight of 20000-100000, an optimum pH of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.5-9.5 and substrate specificity for L-N-acetylphosphinothricin (L-Acetylphosphinothricin (L-Acetylphosphinothricin (L-Acetylphosphinothricin (L-Stepselective production of L-phosphinothricin (PPT) and for inducing reversible male scrility in plants (PPT inhibits the enzyme glutamine synthase in anthers). The deacetylase comprises at least one of four sequences (See AAR61321-24) (Updated on 2s-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein, treatment, prevention, protein therapy, AIDS; gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; developmental abnormality; fetal deficiency; blood disorder; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                   Deacetylase, enzyme, L-N-acetylphosphinothricin, L-AcPPT,
L-phosphonothricin; PPT; glutamine synthase; plant; male sterility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4;
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75.0%; Pred. No. 1.4e+06;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brevundimonas diminuta; (mixed culture).
Nocardia globerula; (mixed culture).
Calulosimicrobium cellulans; (mixed culture).
Agrobacterium tumefaciens; (mixed culture).
                                                                                                                                                                                                                                                                                                                                                                                                                                                paradoxus; (mixed culture)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY07986 standard; protein; 5 AA.
AAR61324 standard; peptide; 4 AA
                                                                                                                                                                                                                                                           Fragment of deacetylase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93DE-04308061.
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                                                                                                                                                                                            (first entry)
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                                                                                                                             (revised)
(revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-286683/36.
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es 3; Conserv
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1 VMAK
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                                                                                                                          16-OCT-2003
25-MAR-2003
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                                                                  AAR61324;
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Best Local S:
Matches
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This invention describes novel isolated human genes and the secreted proteins they encode. The products of the invention are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polymetries in a sample or by determining the presence of mutations in the new polymucleotides. Dased on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, schizophrenia, prostate allergies, Alzheimer's and cognitive disorders, pulmonary disorders, classed means asser, skebtatal or cardiac muscle disorders, pulmonary disorders, controlled the controlled the cardiac muscle disorders, pulmonary disorders, controlled the cardiac muscle disorders, pulmonary disorders, controlled the cardiac muscle disorders, pulmonary disorders, controlled the cardiac muscle disorders, pulmonary disorders, controlled the cardiac muscle disorders, pulmonary disorders, controlled the cardiac muscle disorders, pulmonary disorders, controlled the cardiac muscle disorders, pulmonary disorders, controlled the cardiac muscle disorders, pulmonary disorders, controlled the cardiac muscle disorders, pulmonary disorders, cardiac muscle disorders, pulmonary disorders, cardiac muscle disorders, pulmonary disorders, cardiac muscle disorders, pulmonary disorders, cardiac muscle disorders, pulmonary disorders, cardiac muscle disorders, pulmonary disorders, cardiac muscle disorders, pulmonary disorders, cardiac muscle disorders, cardiac muscle disorders, cardiac muscle disorders, cardiac muscle disorders, cardiac muscle disorders, cardiac muscle disorders, cardiac muscle disorders, cardiac muscle disorders, cardiac muscle disorders, cardiac muscle disorders cardiac muscle disord
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immune system disease; autoimmune disease; hepatic disease; lymphoma; renal disease; inflammation; allergy; Alzheimer's disease; schizophrenia; cognitive disorder; prostate disease; skeletal; cardiac; muscle disorder; pulmonary disorder; transplant rejection; osteoclast; osteoporosis; arthritis; malignancy; digestive; endocrine; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplant rejection, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, digestive/endocrine disorders, infections and AIDS. The human secreted proteins of the invention are represented in AAVO7852-VO793 and the encoding nucleic acids are represented in AAX37451-X37552
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A, Feng P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes and the secreted polypeptides they encode
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, Endress GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14; DB 2; Length 5; Pred. No. 1.4e+06; 3; Mismatches 0; Indels
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Carter KC,
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, Yu G, Janat F, Ni J,
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97US-0060837P.
97US-0060837P.
97US-0060838P.
97US-0060843P.
97US-0060862P.
97US-0060862P.
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40.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0060880P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-264022/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferrie AM, Yu G, C
Lafleur DW, Shi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                   Homo sapiens
                                                                                                                                                                                              WO9918208-A1
                                                                                                                                                                                                                                                                                               01-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-1997;
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02-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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The present sequence represents an immunisation motif normally excluded, but which may be used with advantage for tolerisation by itself or in conjunction with other epitope sequences from the present invention. The present invention describes a polypeptide comprising a human myelin basic protein (hMBP) fragment including P89-101 of hMBP, excluding native hMBP. The term P89-101 is not defined but may be intended to mean amino acids 89-101 of hMBP. The polypeptide can be used for tolerising a mammalian host immune system comprising and T cells to an immunogen of interest, wherein said immunogen is restricted by a transplantation antigen of said
                                                                                                                                                                             The inventors claim recombinant penicillin acyltransferase (PAT) and DNA coding for PAT. PAT catalyses the last step in the biosynthesis of penicillin G and penicillin V. More specifically, the coding strand of the DNA has the nucleotide sequence shown below. This includes three introns and codes for a PAT protein with mol. wt. ca. 40kD. Plasmid vectors pBC2001 and pBC2002 are specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide comprising human myelin basic protein fragment - useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myelin basic protein; immunity; immune response; neurological; T-cell; human; immunogen; B-cell; transplantation antigen; immunomodulator.
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                       Recombinant penicillin acyl-transferase - and DNA coding for it
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                                                                                                                                                                                                                                                                                                                                               Length 4;
                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                            61.9%; Score 13; DB 1; Le
100.0%; Pred. No. 1.4e+06;
Live 0; Mismatches 0;
                                    ö
                                    Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunisation motif associated with AChR 1.
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                                    Palma N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW55770 standard; peptide; 4 AA.
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                                                                                                                                               Claim 9; Page 48; 52pp; English.
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(first entry)
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(BIOC ) BIOCHEMIE GMBH.
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                                      Leitner
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                                                                      WPI; 1989-294357/41.
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                             Sequence 4 AA;
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08-JUL-1998
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                                                                                         in tolerization alone or in association with epitopes to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences will normally be part of 9-15 amino acid sequence, excluded as motifs for immunisation but useful in tolerisation. . (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                based on the amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence of fragment 21, the tryptic fragment of recombinant penicillin acyltransferase (PAT) polypeptide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                               Autoantigen; MBP; myelin basic protein; transplantation antigen; myasthenia gravis; myasthenics; Transplantation antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligopeptide and polypeptide compsns. - based on the amino of an immunogen and used for modulating the immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 61.9%; Score 13; DB 1; Length 4; Best Local Similarity 50.0%; Pred. No. 1.4e+06; Matches 2; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penicillin biosynthesis; enzyme; antibiotic
                                                                                                                                                                                                                                                                                                                                                                                  (STRD ) UNIV LELAND STANFORD JUNIOR.
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88AT-00002201.
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                                    (revised)
(first entry)
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                                                                                                            acetyl choline receptor.
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LVAK 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4 AA;
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                                                                                         Motif useful
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08-SEP-1988;
                                  25-MAR-2003
09-JUL-1990
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                                                                                                                                                                                                      Synthetic.
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 AAP91629;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modulating or tolerizing the immune system, useful for treating multiple sclerosis, by administering a peptide derived from human myelin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel method for modulating or tolerizing the
 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-
                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                        MBP; myelin basic protein; human; tolerance; immune system; multiple sclerosis; autoimmune response; autoimmune disease; immunosuppressive; neuroprotective.
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Pred. No. 1.4e+06;
2; Mismatches 0; Indels
                                                                      Score 13; DB 2; Length 4;
Pred. No. 1.4e+06;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                               Human MBP protein derived peptide SEQ ID 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 14; 21pp; English
                                                                                                                                                                                                                           ABB84333 standard; peptide; 4 AA.
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90US-00517245.
91WO-US002991.
92US-008774444.
93US-00066325.
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50.0%;
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50.0%;
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host. (Updated on 25-MAR-2 2003 to correct PR field.)
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Best Local Similarity 50.0
Matches 2; Conservative
                                                                                 Similarity 50.0
2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEINMAN L. ZAMVIL S.
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                                                                                                                             2 VIAK 5
                                          Sequence 4 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1991;
30-APR-1992;
21-MAY-1993;
22-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steinman L,
                                                                                                                                                                                                                                                                                   17-0CT-2002
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01-MAY-1990;
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                                                                                                                                                                                                                                                        ABB84333;
                                                                     Query Match
Best Local
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                                                                                               Matches
                                                                                                                                                                                                RESULT 14
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muclaic acid polymerase or aderivative nucleic acid polymerase with a muclaic acid polymerase or aderivative nucleic acid polymerase with a mutation that decreases 5-3' exonuclease activity or that reduces discrimination against dideoxynucleotide triphosphates. Also described:

(1) a vector comprising the nucleic acid (1); (2) a host cell comprising the nucleic acid (1); (3) a nucleic acid polymerase or its derivative; (4) a kit comprising a nucleic acid polymerase or its derivative; of (3); (5) making the nucleic acid polymerase of (3); (6) synthesising a DNA; (7) thermocyclic amplification of nucleic acid; and (8) primer amplification, reverse transcription, RNA amplification or primer extension reactions. The present sequence represents a Thermus oshimai nucleic acid polymerase peptide, which is given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an isolated nucleic acid (I) encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid, useful for DNA sequencing or amplification, reverse transcription, RNA amplification or primer extension reactions.
                                                                                                                                                                                                            Thermus oshimai nucleic acid polymerase peptide 704-707 SEQ ID NO:26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                              Thermus oshimai; nucleic acid polymerase; enzyme; DNA sequencing; amplification; reverse transcription; RNA amplification;
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                                                                                               ABR57300 standard; peptide; 4
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                    primer extension.
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1 LVAK 4
                                                                                                                                                                                                                                                                                                                        Thermus oshimai.
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                                                                                                                                                                         09-SEP-2003
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Sequence 16, Appl
Sequence 20, Appl
Sequence 24, Appl
Sequence 329, App
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8, Appli
12, Appl
                                                                                                                      August 12, 2004, 06:54:59; Search time 41 Seconds (without alignments) 38.284 Million cell updates/sec
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| Can2 6 ptodata 2 pubpaa / US07 PUBCOMB.ppp:*
| Can2 6 ptodata 2 pubpaa / US06 PUBCOMB.ppp:*
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| Can2 6 ptodata 2 pubpaa / US06 PUBCOMB.ppp:*
| Can2 6 ptodata 2 pubpaa / US08 PUBCOMB.ppp:*
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| Can2 6 ptodata 2 pubpaa / US10B PUBCOMB.ppp:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-862-145A-1
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US-09-862-145A-12
US-09-862-145A-16
US-09-862-145A-20
US-09-862-145A-24
US-10-195-730-329
US-10-195-730-329
US-10-402-029-4
US-10-402-029-12
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US-10-285-108A-4
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                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Sequence 24, Appl
Sequence 33, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 31, Appli
Sequence 163, Appl
Sequence 163, Appl
Sequence 163, Appl
Sequence 163, Appl
Sequence 11, Appl
Sequence 11, Appli
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Sequence 20, Appl
Sequence 5, Appli
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Sequence 28,
Sequence 37,
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               Sequence Sequence
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S US-10-285-108A-8

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US-10-285-108A-26

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US-10-285-108A-26

US-10-285-108A-27

US-00-484-409-33

US-00-797-543-3

US-00-797-543-3

US-00-797-543-3

US-00-759-163

US-00-759-163

US-00-759-163

US-00-759-163

US-00-759-163

US-00-759-163

US-00-759-163

US-10-087-905-6

US-10-087-905-6

US-10-087-905-6

US-10-087-905-6

US-10-087-905-6

US-10-087-905-6

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US-10-087-905-6

US-10-087-905-6

US-10-087-905-6

US-10-087-905-6

US-10-087-918-7-805-6

US-09-764-226-3

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US-09-764-226-3
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US-09-562-912-4
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## ALIGNMENTS

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Sequence 4, Application US/09992124A
Publication No. US20030162289A1
GENERAL INFORMATION:
APPLICANT: Heidaran, Mohammad A.
APPLICANT: Heidaran, Jamie H.
APPLICANT: Haland, Perry D.
APPLICANT: Cambell, Robert L.
ITILE OF INVENTION: Peptides Promoting Cell Adherence, Growth and Secretion.
FILE REFERENCE: 102-410
CURRENT APPLICATION NUMBER: US/09/992,124A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 70
SOFTHARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Synthetic peptide selected for biological activity US-09-992-124A-4
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Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 0;
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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LENGTH: 5
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Publication No. US2003013838A1
GENERAL INFORMATION:
APPLICANT: Sciberg, Miri
APPLICANT: Shapiro, Stanley
TITLE OF INVENTION: Peptides and the Use Thereof in Darkening the Skin
FILE REPREBNICE: J&J-1991
CURRENT APPLICATION WUMBER: US/09/862,145A
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Version 3.1
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Seiberg, Miri
APPLICANT: Seiberg, Miri
APPLICANT: Shaplro, Stanley
TITLE OF INVENTION: Peptides and the Use Thereof in Darkening the Skin
FILE REPERENCE: J6J-1991
CURRENT APPLICATION NUMBER: US/09/862,145A
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 24
SEQ ID NOS: 24
SEQ ID NO 8
LENGTH: 5
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APPLICANT: Seiberg, Miri
APPLICANT: Shapiro, Stanley
TITLE OF INVENTION: Peptides and the Use Thereof in Darkening the Skin
FILE REFERENCE: J&L-1991
CURRENT APPLICATION NUMBER: US/09/862,145A
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
SEQ ID NO. 4
LENGTH: 5
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60.0%; Pred. No. 1.2e+06;
iive 1; Mismatches 1;
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Pred. No. 1.2e+06;
1; Mismatches 1;
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LOCATION: (5)..(5)

OTHER INFORMATION: C-terminal Amidation
MS-09-862-145A-4
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 60.0%,
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Matches 3, Conservative
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1 SLIGK 5
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1 SLIGK 5
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Sequence 20, Application No. US20030138388A1

GENERAL INFORMATION:

APPLICANT: Selberg, Miri

APPLICANT: Shapiro, Stanley

TITLE OF INVENTION: Peptides and the Use Thereof in Darkening the Skin

FILE REPREBUCE: J&J-1991

CURRENT APPLICATION NUMBER: US/09/862,145A

CURRENT FILING DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 20

LENGTH: 5
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Sequence 16, Application US/09862145A

Publication No. US20030138388A1

GENERAL INFORMATION:
APPLICANT: Shapiro, Stanley
TITLE OF INVENTION: Peptides and the Use Thereof in Darkening the Skin
FILE REFERENCE: J62-1991

CURRENT PILION DATE: 2001-05-21

CURRENT PILION DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 16

TENDER OF SEQ ID NOS: 24

SEQ ID NO 16
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60.0%; Pred. No. 1.2e+06;
iive 1; Mismatches 1;
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Pred. No. 1.2e+06;
1; Mismatches 1;
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LOCATION: (1). . (1)
OTHER INFORMATION: Palmitoyl N-terminus
                     FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(1)
OTHER INFORMATION: Palmitoyl N-terminus
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| NAME/KEY: MISC FEATURE
| LOCATION: (5)...(5)
| OTHER INFORMATION: Amidated C-terminus
US-09-862-145A-12
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OTHER INFORMATION: Synthetic Peptide
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Best Local Similarity 60.0%;
Matches 3; Conservative
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Gaps
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US-10-402-029-8

; Sequence 8, Application US/10402029

; Publication No. US20040005288A1

; GENERAL INPORMATION:

; APPLICANT: Lin, Comie

; APPLICANT: Lin, Comie

; APPLICANT: Selberg, Miri

; FILE REFERENCE: JGJ-2099

; CURRENT APPLICATION NUMBER: US/10/402,029

; CURRENT FILING DATE: 2003-03-28

; NUMBER OF SEQ ID NOS: 30

; SEQ ID NO S: 30

; SEQ ID NO E
                                                                                                                                                           66.7%; Score 14; DB 14; Length 5; 40.0%; Pred. No. 1.2e+06; Live 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10402029
Publication No. US20040005288A1
GENERAL INFORMATION:
APPLICANT: Lin, Connie
APPLICANT: Selberg, Miri
TITLE OF INVENTION: Compositions for Darkening the Skin
FILE REFERENCE: UK-2099
CURRENT APPLICATION NUMBER: US/10/402,029
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%; Score 14; DB 15; Length 5; 60.0%; Pred. No. 1.2e+06; Live 1; Mismatches 1; Indels
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    CTHER INFORMATION: C-terminal Amidation
US-10-402-029-4
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                            Query Match
Best Local Similarity 40.uv
Local 2; Conservative
NUMBER OF SEQ ID NOS: 390
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 329
LENGTH: 5
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                                                                                 TYPE: PRT
CORGANISM: Homo sapiens
US-10-195-730-329
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1 SMVSK 5
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1 SLIGK 5
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US-10-402-029-4
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TITLE OF INVENTION: Peptides and the Use Thereof in Darkening the Skin
FILE REFERENCE: 1&c-1986
CURRENT APPLICATION NUMBER: US/09/862,145A
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
SEQ ID NO 24
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Publication No. US2030014492A1
GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: 101 Human Secreted Proteins
FILE REFERENCE: PZ017P1
CURRENT APPLICATION NUMBER: US/10/195,730
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: US/9/281,976
PRIOR PRILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/060,837
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
                                                                      FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1) - (1)
OTHER INFORMATION: Stearatoyl N-terminus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (5) . (5)
OTHER INFORMATION: Stearatoyl C-terminus
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DOCATION: (1)...(1)
OTHER INFORMATION: Stearatoyl N-terminus
US-09-862-145A-24
                                    FEATURE: OTHER INFORMATION: Synthetic Peptide
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OTHER INFORMATION: Synthetic Peptide
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APPLICANT: Seiberg, Miri
              ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 3; Conservative
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Matches 3; Conservative
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APPLICANT: Seiberg, Miri
TILLE OF INVENTION: Compositions for Darkening the Skin
FILL REPERENCE: 420-2099
CURRENT APPLICATION NUMBER: US/10/402,029
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3:1
SEQ ID NO 24
LENGTH: 5
                                                                                                                                                                                                                                 APPLICANT: Lin, Connie
APPLICANT: Seiberg, Miri
TITLE OF INVENTION: Compositions for Darkening the Skin
FILE REFERENCE: J&J-2099
CURRENT APPLICATION NUMBER: US/10/402,029
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 5
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60.0%; Pred. No. 1.2e+06;
cive 1; Mismatches 1;
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OTHER INFORMATION: Stearatoyl N-terminus
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LOCATION: (1)...(1)
OTHER INFORMATION: Stearatoyl N-terminus
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                                                                                                                                                                        Sequence 20, Application US/10402029
Publication No. US20040005288A1
GENERAL INFORMATION:
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Publication No. US2004005288A1
GENERAL INFORMATION:
APPLICANT: Lin, Connie
APPLICANT: Selberg, Miri
TITLE OF INVENTION: Compositions for Darkening the Skin;
FILE REFERENCE: J&-2099
CURRENT APPLICATION NUMBER: US/10/402,029
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH 5
LENGTH 5
LENGTH 6
NO 12
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APPLICANT: Seiberg, Miri
TITLE OF INVENTION: Compositions for Darkening the Skin
FILE REFERENCE: J&J-2099
CURRENT APPLICATION NUMBER: US/10/402,029
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
LENGTH: 5
    Pred. No. 1.2e+06;
1; Mismatches 1;
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LOCATION: (1). \(\tilde{\pi}\) (1)
OTHER INFORMATION: Palmitoyl N-terminus
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OTHER INFORMATION: Palmitoyl N-terminus
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; NAME/KEY: MISC FEATURE
; LOCATION: (5)...(5)
; OTHER INFORMATION: Amidated C-terminus
US-10-402-029-12
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ORGANISM: Artificial Sequence
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S SQUENCE 4, Application US/10285108A

S SQUENCE 4, Application US/10285108A

S GQUENCE 4, Application US/10285108A

S GQUENCAL INFORMATION:

APPLICANT: Ini, Connie

APPLICANT: Mu, Jane Connie

APPLICANT: Mu, Jane Connie

APPLICANT: Mu, Jane Connie

APPLICANT: Mu, Jane Connie

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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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(c) 1993 - 2004 Compugen Ltd.
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US-09-061-768A-5 US-09-142.334-29 US-08-843-306B-18 US-08-848-673B-49 US-08-964-747-4 US-09-764-246-5 5217869-4 US-08-014-979-18 US-08-142-439A-8 US-08-142-439A-8 US-08-142-439A-8 US-08-142-439A-8 US-08-142-439A-8 US-08-142-431A-8 US-08-869-477-8 US-08-869-477-8 US-08-869-477-8 US-08-869-477-8 US-08-869-477-8 US-08-869-477-8 US-08-869-477-8 US-08-869-477-8 US-08-869-477-8 US-08-869-477-8 US-08-869-477-8 US-08-869-477-8 US-08-869-477-8 US-08-869-477-8 US-08-869-477-8 US-08-869-477-8	WENTS  TORS OF THE P33  FULE REGULATORY  E7 ONCOPROTEIN  A  A  16	B 1; +05; s
2448833334 1244883333 124444434 12586434444434 1268644434 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864443 126864444 126864444 126864444 126864444 126864444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 12686444 1268644 12686444 12686444 12686444 12686444 12686444 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 1268644 126864 1268644 1268644 1268644 1268644 1268644 1268644 1268644	MEN MEN ORE	U
00000000000000000000000000000000000000	plication US/08193977  MATION: WEBSTER, KEVIN R. COLEMAN, KEVIN G. COLEMAN, KEVIN G. FENTION: PAPLILOMAVIRUS GUUNCES: 34  CERTION: PAPLILOMAVIRUS GUUNCES: 34  CERTION: PAPLILOMAVIRUS UNITED STATES OF AMERICA UNITED STATES OF AMERICA UNITED STATES OF AMERICA UNITED STATES OF AMERICA SYSTEM: PATONIN STREET DABLE FORM: PATONIN STREET SYSTEM: PATONIN STREET SYSTEM: PATONIN STREET SYSTEM: NN NUMBER: US/08/193,977 SYSTEM: NN NUMBER: 33,208 SYSTEM: NN NUMBER: 33,208 SYSTEM: NN NUMBER: 33,208 SYSTEM: NN NUMBER: 33,208 SYSTEM: NN NUMBER: 33,208 SYSTEM: NN NUMBER: 33,208 SYSTEM: NN NUMBER: 33,208 SYSTEM: NN NUMBER: 33,208 SYSTEM: NN NUMBER: 33,208 SYSTEM: NN NUMBER: 33,208 SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM: SYSTEM	Score 13; Pred. No.; Mismat;
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	HIT I 18-193-977-16	61. 50. vative
	Licati 111 110N: BESTER BESTER ADDES ADDES ADTON: ADDES ADTON: ADDES ADTON: ADDES ADTON: ADDES ADTON: ADDES ADD	<i>≻</i> , <i>i</i> ,
20000000000000000000000000000000000000	T 1 193-977-16 uence 16, Application ent No. 5625031 APPLICANT: WEBSTER, K APPLICANT: WEBSTER, K APPLICANT: COLEMAN, K TITLE OF INVENTION: P TITLE OF INVENTION: P TITLE OF INVENTION: P TITLE OF INVENTION: P TITLE OF INVENTION: P TITLE OF INVENTION: P TITLE OF INVENTION: P TITLE OF INVENTION: P TITLE OF INVENTION: P TITLE OF INVENTION: P TITLE OF INVENTION: P TITLE OF INVENTION: P TITLE OF INVENTION: P TITLE OF INVENTION OF THE OF	Similaritications Simple Singl
	16, Appl 16, Appl 10, Se2503 10, Se2503 10, Se2503 10, Se2503 10, Se2503 10, Tuven 10, Tuven 10, Tuven 10, Tuven 10, Se203 11, Se20	Sim 2; 2 VI 2 VI 2 IM
	T. I 193-977-16 UBERL NO. 5625 WERAL INFORMT: APPLICANT: TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TOWNERS OF SECONDERS. COMPUTER: CA. COMPUTER: CA. COMPUTER: CA. COMPUTER: CA. COMPUTER: CA. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE OF INV. TITLE COMPUTER: CA. TITLE COMPUTER: CA. TITLE COMPUTER: CA. TITLE COMPUTER: CA. TITLE COMPUTER: CA. TITLE COMPUTER: CA. TITLE COMPUTER: CA. TITLE COMPUTER: CA. TITLE COMPUTER: CA. TITLE COMPUTER: CA. TITLE COMPUTER: CA. TITLE COMPUTER: CA. TITLE CA. TITLE COMPUTER: CA. TITLE CA.	Matc local
00000000000000000000000000000000000000	ALIT US-08-193-977-16 Sequence 16, Application US/08193977 Patent No. 5625031 PAPPLICANT: WEBSTER, KEVIN R. APPLICANT: WEBSTER, KEVIN G. TITLE OF INVENTION: PAPTILIOMAVIRU, TITLE OF INVENTION: PAPTILIOMAVIRU, TITLE OF INVENTION: PAPTILIOMAVIRU, MUMBER OF SEQUENCES: 34 CORRESPONDENCE ADDRESS: ADDRESSEE: REED & ROBINS STREET: 635 BRYANT STREET CITY: PALO ALTO STRATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICALPONITY: UNITED STATES OF AMERICALION TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: BALGHIN RE-BASH E PORTION: COMPUTER: BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: BALGHIN RE-BASH E STATE CLASSIFICATION NUMBER: 3208 STILING BATE: 08 FEB-1994 CLASSIFICATION NUMBER: 33208 REFERENCE/DOCKET NUMBER: 5998-0 TELECOMMUNICATION INFORMATION: RAME: ROBINS, ROBERTA A. REGISTRATION SOFT STATES TELERHONE: (415) 327-3231 INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 5 amino acid STYPE: amino acid STYPE: amino acid STYPE: amino acid TYPE: amino acid STYPE: amino acid TYPE: peptide	Query Match Best Local S Matches 2
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Mismatches
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REGISTRATION NUMBER: 36,113
REPERENCE/DOCKET NUMBER: 003300-286
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 67:
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100.0%; Pred
0; M
                                                                                                                               ; Sequence 67, Application US/07969305; Patent No. 5609872
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Best Local Similarity
3; Conserve
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                                                                                                                                                                                                                                                                                 61.9%; Score 13; DB 6; Length 5; 75.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUDRESSEE: Burns, Doane, Swecker & Mathis STREET: George Mason Bidg., Washington & Prince Sts. CITY: Alexandria STATE: Virginia
                                                                      APPLICANT: KAUVAR, LAWRENCE M.
TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,305
FILING DATE: 08-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: AHLBORG, NIKLAS
APPLICANT: BERZINS, Klavs
APPLICANT: PERLAANN, Peter
TITLE OF INVENTION: NEW PEPTIDES AND THEIR USE
NUMBER OF SEQUENCES: 70
CORRESSED SIDNESS:
ADDRESSEE: BURNS, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION ...
FILING DATE: 08-APR-1993
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9002684-0
FILING DATE: 17-AUG-1990
ATTOMNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REGISTRATION NUMBER: 36,113
REGISTRATION NUMBER: 003300-28
TELECOMUNICATION INFORMATION:
"""RELECOMUNICATION INFORMATION:
"""", REPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           003300-286
                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/255,906
FILING DATE: 11-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Virginia
COUNTRY: United States
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDAPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 66, Application US/07969305
Patent No. 5609872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 amino acids
                                                                                                                             NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: peptide US-07-969-305-66
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Best Local Similarity
Matches 3; Conserv
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             RESULT 2
5217869-19
;Patent No. 5217869
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5217869-19
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Sequence 124, Application US/08456424

Sequence 124, Application US/08456424

Patent No. 5807979

PAPLICANT: SATTERTHWAIT JR., ARNOLD C.

APPLICANT: ARRHENIUS, THOMAS

APPLICANT: CABEZAS, EDELMIRA

TITLE OF INVENTION: SYMTHETIC, STABILIZED, THREE-DIMENSION

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 145

CORRESPONDENCE ADDRESS:

ADDRESSE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4;
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GENERAL INFORMATION:

APPLICANT: ALLBORG, Niklas

APPLICANT: BERZINS, Klavs

APPLICANT: BERZINS, Klavs

APPLICANT: BERZINS, Ravs

APPLICANT: BERZINS, Ravs

TITLE OF INVENTION: NEW PEPTIDES AND THEIR USE

NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: George Mason Bldg., Washington & Prince Sts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Alexandria
STATE: Virginia
STATE: Virginia
COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATENT PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,305
FILING DATE: 08-APR-1993
CLASSICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION NUMBER: SS 9002684-0
FILING DATE: 17-AUG-1990
ATTONEY/AGENT INFORMATION:
AMAME: CLASSICATION CONTROL FOR AUG-1990
ATTONEY/AGENT INFORMATION:
AMAME: CLASSICATION CONTROL FOR AUG-1990
ATTONEY/AGENT INFORMATION:
AMAME: CLASSICATION CONTROL FOR AUG-1990
ATTONEY/AGENT INFORMATION:
AMAME: CLASSICATION CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUGHLIAND CONTROL FOR AUG
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Pred. No. 3e+05;
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Patent No. 6245884

GENERAL INFORMATION:

APPLICANT: HOOK, VIVIAN Y.H.

TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA

TITLE OF INVENTION SECRETASES RELATED TO ALZHEIMER'S DEMENTIA

CURRENT APPLICATION NUMBER: US/09/173,887

CURRENT FILING DATE: 1998-10-16

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                 FILING DATE: ABANDONING
CLASSIFICATION: 435
APPLICATION NUMBER: PCI/US/91/02650
FILING DATE: 18-APR-1991
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/510,706
FILING DATE: 18-APR-1990 (ABANDONED)
CLASSIFICATION: 435
APPLICATION NUMBER: 32,165
ATTONNEY/AGENT INNORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REBERENCE/DOKERT NUMBER: UTSD: 432/PAR
TELEFRANCATION INFORMATION:
TELEFRANCATION INFORMATION:
TELEFRANCATION INFORMATION:
TELEFRANCATION INFORMATION:
TELEFRANCATION OF SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
TENNGTH: 4 amino acids
                                                            UMBER: US 07/822,011
ABANDONED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-842-306B-19;
Sequence 19, Application US/08842306B
Patent No. 6271197;
GENERAL INFORMATION:
                        FILLING DATE: 16-FEB-1993
CLASSIFICATION: 435
APPLICATION NUMBER: US 0'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 10U..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-429-964-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-173-887-3
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| Patent No. 5952233
| GENERAL INFORMATION:
| APPLICANT: BROWN, MICHAEL S.
| APPLICANT: BROWN, MICHAEL S.
| APPLICANT: REISS, YUVAL.
| APPLICANT: REISS, YUVAL.
| APPLICANT: TRIES, YUVAL.
| TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL.
| TITLE OF INVENTION: TRANSFERASE INHIBITORS
| NUMBER OF SEQUENCES: 85
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: ARNOLD, WHITE & DURKEE
| STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,964
FILING DATE: 27-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,424
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
APPLICATION NUMBER: US 07/866,040
FILING DATE: 08-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, KARL
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 278022000120
TELEPHONE: 415-813-5600
TELEPHONE: 415-84-0792
                                                   COUNTK::
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Propsy disk
MEDIUM TYPE: Propsy disk
MEDIUM TYPE: Propsy disk
MEDIUM TYPE: Propsy disk
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CLASSIFICATION: 530
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/224,059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UNITED STATES OF AMERICA ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 706141
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 amino acids
                  PALO ALTO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 1; Conserv
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1 IVSK 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                        STATE: CP
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TELEX: 70
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Gaps

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Gaps

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Sequence 11, Application US/09268163B
Sequence 11, Application US/09268163B
Patent No. 6353091
GENERAL INFORMATION:
APPLICANT: Lipscombe, Diane
APPLICANT: Schorge, Stephanie
TITIE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
FILE REFERENCE: B1055/7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-294-887-4

i Sequence 4, Application US/09294987

j Sequence 4, Application US/09294987

j Sequence 4, Application US/09294987

j GENERAL INFORMATION:

j APPLICANT: HOOK, Vivian Y.H.

j TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIAN

j CURRENT APPLICATION NUMBER: US/09/294,987

j CURRENT FILING DATE: 1999-04-20

j PRIOR APPLICATION NUMBER: US 09/173,887

j PRIOR FILING DATE: 1998-10-16

j NUMBER OF SEQ ID NOS: 6

j SEQ ID NO 4

j FRION 0 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12; DB 3; Length 4;
; Pred. No. 3e+05;
0; Mismatches 0; Indels
                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                   CURRENT APPLICATION DATE:

CURRENT APPLICATION NUMBER: US/08/838,9738
FILING DATE: 2-Apr-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/631,319
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P
REGISTRATION UNDER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-838-973B-17
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                             TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.1%; S
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
; ORGANISM: mammalian
US-09-294-987-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VIA 4
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US-09-268-163-11
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                                                                                  TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS, AND USES RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02109-2770.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordchad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,306B
FILING DATE: 23-Apr-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/771,212
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: US 08/771,319
FILING DATE: 11-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MIV-074.04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEPA: 617-832-1000
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT Berlin, Vivian
Bamagnez, Veronique
Smith, Susan
TITLE OF INVENTION: ASSAYS AND REAGENTS
ANTI-FUNGAL AGENTS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.1%; Score 12; DB 100.0%; Pred. No. 3e+rative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-08-842-3068-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/08838973B Patent No. 6277564 GENERAL INFORMATION:
                                            Damagnez, Veronique
Smith, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
  Levin, David
Ohya, Yoshikazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 48
                                                                                                                               NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston STATE: MA
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Best Local Similarity
Matches 3; Conserva
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NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 4
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75.08;
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ORGANISM: Artificial Sequence
                                                                                                                                                    Query Match
Best Local Similarity 75.0°
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-601-178-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                            2 VIAK 5
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US-09-665-362A-18
                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-797-543-3
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                                                                                                                                                                                                                      57.1%; Score 12; DB 4; Length 4; 100.0%; Pred. No. 3e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LUKE, Richard William Arthur APPLICANT: COTTON, Ronald APPLICANT: COTTON, Ronald COTTON, ROHAGE COTTON, PEPTIDE DERIVATIVES FILE REFERENCE: 1991-174
CURRENT APPLICATION NUMBER: US/09/308,175A
CURRENT FILING DATE: 1999-05-17
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-27
NUMBER OF SEQ ID NOS: 22
SOFFWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ADMON, Arie
APPLICANT: PALTIELI, Yoav
APPLICANT: PALTIELI, Yoav
APPLICANT: PALTIELI, SILVIA
APPLICANT: SILOTXY, RONI;
TITLE OF INVENTION: PLACENTAL PROTEIN 13
FILE REFERENCE: ADMON=1
CURRENT APPLICATION NUMBER: US/09/601,178
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: PCT/1L99/00036
PRIOR FILING DATE: 1999-01-21
PRIOR RILING DATE: 1998-01-29
CURRENT APPLICATION NUMBER: US/09/268,163B
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: US 60/077,901
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-308-175A-8
; Sequence 8, Application US/09308175A
; Patent No. 6355617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09601178
Patent No. 6548306
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                            TYPE: PRT
ORGANISM: Conus geographus
                                                                                                                                                                                                                                       Similarity 100.
3; Conservative
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Best Local Similarity 66.7
Poservative 2; Conservative
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1 VAK 3
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Best Local S:
Matches 3
                                                                                                                               LENGTH: 4
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Patent No. 6627409

GENERAL INFORMATION:

APPLICANT: HOOK, VIVIAN Y. H.

TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA

FILE REFERENCE: P-AS 4579

CURRENT APPLICATION NUMBER: US/09/797,543

CURRENT FILING DATE: 2001-05-29

PRIOR PLING DATE: 1998-10-16

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/09665362A

Fatent No. 6632626

GENERAL INFORMATION:
APPLICANT: BROWN MICHAEL S.
APPLICANT: BROWN MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL
ITLE OF INVENTION: METHODS OF ASSAYING FARNESYL TRANSFERASE
FILE REFERENCE: UTSD: 249 USD1.
CURRENT FILING DATE: 2003-07-22
PRIOR FILING DATE: 1992-12-22
PRIOR FILING DATE: 1992-11-20
PRIOR FILING DATE: 1990-11-20
SPRIOR FILING DATE: 1990-11-20
SOFTWARE: PATENTIN VOWER: 07/510,706
SPRIOR FILING DATE: 1990-11-20
SOFTWARE: PATENTIN VOY: 2.1
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      Length 4;
Score 12; DB 4
Pred. No. 3e+05
0; Mismatches
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us-09-890-463-1.closed.rai

Query Match 57.1%; Score 12; DB 4; Length 4; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 3; Conservative 0; Mismatches 0; Indels US-09-665-362A-18

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0; Gaps

2 VIA 4 ||| 2 VIA 4

Op δ

Search completed: August 12, 2004, 06:55:49 Job time : 19 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 12, 2004, 07:01:35; Search time 37 Seconds (without alignments) 44.196 Million cell updates/sec

US-09-890-463-2 83 1 SVIAKQMTYKVYMSGTV 17 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2990 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 17

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	scr	24K antigen - Myco	gamma V-J	kotriene B-	V-D-J	Н	al prote	urease (EC 3.5.1.5	_	S	ferredoxin al - Ja	S	C	tical pro		-cell recept	34100046	Iq H chain V-D-J r	plastocvanin - Mic	15K protein 5106 -	TcR gamma V-J regi	malate dehydrogena	Iq lambda chain J	erine pro		disaggregatase - M	rotein OF200020	oligo-1.6-glucosid	lucosidase	luca
SUMMARIES		 																												
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	-1993	cobacterium]			10 sdr		
	C;Species: Mycobacterium bovis C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 18-Jun-1993 C;Accession: B60278	R.Fifis, T.; Costopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R. Infect. Immun. 59, 800-807, 1991 A; Title: Purification and characterization of major antigens from a Mycobacterium b	900061		<pre>i Length 16; 02; 3; Indels 0; Gaps</pre>		
ovis (fragment)	s _revision 11-Dec-1992	Radford, A.J.; Bacio 1991 racterization of majo	UID:91147217; PMID:19		31.3%; Score 26; DB 2; Length 16; 55.6%; Pred. No. 3.4e+02; ive 1; Mismatches 3; Indels		
B60278 860278 24K antigen - Mycobacterium bovis (fragment)	C;Species: Mycobacterium bovis C;Date: 11-Dec-1992 #sequence C;Accession: B60278	Rifitis, T.; Costopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R. Infect. Immun. 59, 800-807, 1991 A;Title: Purification and characterization of major antigens from	A;Reference number: A60278; M A;Accession: B60278 A;Status: preliminary	A;Molecule type: protein A;Residues: 1-16 <fif></fif>	Similarity 5; Conservat	B TYKVYMSGT 16	4 TYKEELKGT 12
B60278 24K antig	C;Species C;Date: 1 C;Accessi	R; Fifis, Infect. I A; Title:	A;Referen A;Accessi A;Status:	A, Molecul A, Residue	Query Match Best Local & Matches	δλ	QQ

Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Musculus (house mouse)
Ciscession: C49037
Ribitate: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
Ciscession: C49037
Ribitate: J. Immunol. 22, 491-498, 1992
Airtle: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T Airtle: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T Airtle: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T Airtle: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T Airtle: Molecule type: DNA
Airtle: Molecule type: DNA
Airtle: Sesidues: 1-11 cezzo-Airtle: Call lines
Airtle: Call Session (NCBI) Airtle: Cell lines
Airtle: Sequence extracted from NCBI backbone (NCBIN:90639, NCBIP:90645)

Query Match 26.5%; Score 22; DB 2; Length 11; Best Local Similarity 66.7%; Pred. No. 1.3e+03; Matches 4; Conservative 1; Mismatches 1; Indels

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Gaps

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11 VYMSGT 16 VWMGGT 'n ð g

RESULT 3

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Gaps

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CjAccession: C49215 | NUID: 93084378; PMID: 145235 | THEAL_CHAUGE UD-UAH-2003 |
CjAccession: C49215 | WID: 93084378; PMID: 1452359 | Heal cobacter species A, Accession: C49215 | WID: 93084378; PMID: 1452359 | A, Accession: C49215 | WID: 93084378; PMID: 1452359 | A, Accession: C49215 | WID: 93084378; PMID: 1452359 | A, Accession: C49215 | WID: 93084378; PMID: 94084378;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      photosystem I protein psad - spinach chloroplast (fragment)
C;Species: chloroplast Spinacia oleracea (spinach)
C;Species: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Feb-1997
C;Accession. S09732
R;Ikeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.
FEBS Lett. 263, 274-278, 1990
A;Fitle: Polypeptide composition of higher plant photosystem I complex. Identification o A;Reference number: S09730; MUID:90242987; PMID:2185953
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C;Keywords: chloroplast; photosynthesis; photosystem I; transmembrane protein
                                                                                                                                                                                                           C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Jun.1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession. S78756
R;Graack, H.R.
submitted to the Protein Sequence Database, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      urase (EC 3.5.1.5) large subunit UreB - Helicobacter felis (fragment)
C;Species: Helicobacter felis
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 06-Jan-2003
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-12 <TUR>
A;Experimental source: ATCC 49179
A;Note: sequence extracted from NCBI backbone (NCBIP:119484)
C;Superfamily: urease, alpha subunit; urease 62K chain homology
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Pred. No. 2.1e+03;
4; Mismatches 2; Indels
                                                                                                                                                                          ribosomal protein MRP-L5, mitochondrial - bovine (fragments)
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A, Residues: 1-12;13-17 <GRA>
C, Keywords: mitochondrion
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A;Accession: S78756
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C, Keywords: hydrolase
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IG H chain V-D-J region (clone B-less 30) - mouse (fragment)
IG H chain V-D-J region (clone B-less 30) - mouse (fragment)
C;Species: Mus wusculus (house mouse)
C;Species: Mus wusculus (house mouse)
C;Accession: PHIG16
C;Accession: PHIG16
J Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PHIS80; MUID:93301609; PMID:8315387
leukorriene B-4 12-hydroxydehydrogenase (EC 1.1.1.-) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 17-Mar-1999
C;Ccession: A47421
R;Yccession: A47421
R;Yckomizo, T; Izumi, T; Takahashi, T; Kasama, T; Kobayashi, Y; Sato, F; Taketani, J Biol. Chem. 268, 18128-18135, 1993
A;Nitle: Enzymatic inactivation of leukotriene B-4 by a novel enzyme found in the porcir A;Reference number: A47421; MUID:93352633; PMID:8394361
A;Accession: A47421
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Feb-1994
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Feb-1994
C;Accession: B45895
B;Lee, K.P.; Taylor, C.; Petryniak, B.; Turka, L.A.; June, C.H.; Thompson, C.B.
J. Immunol. 145, 344-352, 1990
A;Title: The genomic organization of the CD28 gene. Implications for the regulation of A;Reference number: A45895; MUID:90293482; PMID:2162892
A;Accession: B45895
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B45895
T-cell surface glycoprotein CD28 short form - human (fragment)
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A;Molecule type: DNA
A;Residues: 1-15 c-15.
A;Experimental source: bone marrow pre-B lymphocyte C;Keywords: immunoglobulin
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Similarity 28.6%;
4; Conservative
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Best Local Similarity 42.95
Matches 6; Conservative
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T-cell receptor gamma chain (2t.23) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: G41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ger A;Reference number: A41946; MUID:92049316; PMID:1658619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein 22947 [imported] - Escherichia coli (strain 0157:H7, substrain EDL93
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R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUD:21074935; PMID:11206551
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A;Experimental source: strain 0157:H7, substrain EDL933
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C;Date: 16-Feb_2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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C;Species: Rhizobium meliloti
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S66458
R;Riedel, K.U.; Jouanneau, Y.; Masepohl, B.; Puehler, A.; Klipp, W.
                                                                                                                                       Gaps
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                                                                                   24.1%; Score 20; DB 2; Length 8; 60.0%; Pred. No. 2.8e+05;
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                                                                                                       Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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Best Local Similarity 50.0%
Matches 4; Conservative
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         A;Molecule type: protein A;Residues: 1-8 <ST2>
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A;Molecule type: DNA
A;Residues: 1-9 <STO>
                                                                                 Query Match
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                                                                                                                                                                                                                                   ferredoxin a1 - Japanese radish (fragments)
C;Species: Kaiware daikon (Japanese radish)
C;Date: 10-Mar_1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
            Gaps
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         Indels
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R; Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M. Arch. Biochem. Biophys. 316, 797-802, 1995
A; Title: Four ferredoxins from Japanese radish leaves.
A; Reference number: S69164; MUID:95168867; PMID:7864635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Note: sequence extracted from NCBI backbone (NCBIP:108592)
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A,Residues: 1-17 <0BA>
C,Keywords: 2Fe-2S; electron transfer; iron-sulfur protein
       2; Mismatches
                                                                                                                                                                                                          talin (glycosylated sites) - chicken (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: gizzard
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Best Local Similarity 42.9'
Matches 3; Conservative
  3; Conservative
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A;Molecule type: protein
A;Residues: 1-8 <STE>
A;Accession: S63494
A;Status: preliminary
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A; Molecule type: protein
A; Residues: 1-17 <HAG>
                                            9 YKVYMS 14
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4 FKTYLS
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RESULT 15
H41946
T-cell receptor gamma chain (5t.12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: H41946
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Ritle: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge A;Receronce number: A41946; MUID:92049316; PMID:1658619
A;Receron: H41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-12 < WHE>
C;Keywords: T-cell receptor
Eur. J. Biochem. 231, 742-746, 1995
A;Title: A Rhizobium meliloti ferredoxin (FdxN) purified from Escherichia coli donates A;Title: A Rhizobium meliloti ferredoxin (FdxN) purified from Escherichia coli donates A;Accession: S66458
A;Accession: S66458
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <RIE>
C;Genetics:
A;Gene: fdxN
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                                                                                                                                                                                                                                                                                         Length 10;
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Best Local Similarity 80.0
Matches 4; Conservative
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4 IIASQXT 10
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Search completed: August 12, 2004, 07:05:39 Job time : 38 secs

11 VYMSG 15 || || || 7 VYSSG 11

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 12, 2004, 06:55:55; Search time 32 Seconds (without alignments) 27.662 Million cell updates/sec

Run on:

1 SVIAKQMTYKVYMSGTV 17 Title: Perfect score: Sequence:

US-09-890-463-2 83

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

943 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 17

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

SwissProt 42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	tion	homo sapien	oryza sativ	microcystis	tenebrio mo	bacillus th	trimeresuru	tenebrio mo	acinetobact	solanum tub	rattus norv	thunnus obe	achatina fu	enterococcu	pseudonaja	saccharomyc	vespula lew	vespa xanth	myoxocephal	alligator m	asaphis dic	pseudonaja	ovis aries	zea mays (m		spinacia ol	tabanus atr	periplaneta	bos taurus	homo sapien	carausius m	heliothis z	tabanus atr	tetrahymena
	Description	P31929	P83466	P10625	P82965	P80072	P82892	P83109	P28467	P81419	P56571	P80978	P35920	P13269	P59072	P99013	P17235	P17234	P20750	P31885	P83246	P59073	P83204	P80633	P81343	P82671	P14595	P04549	32	P04277	38	m	1459	005055
SUMMARIES		ULAD HUMAN	MP2A ORYSA	AS MICAE	ADFA TENMO	LT_BACTQ	21_TRIST	ADFB_TENMO	ACEA_ACICA	ODPB_SOLTU	ES1_RAT	COXI THUOB		CPD1_ENTFA	NXSN_PSETE	UXB2_YEAST	CRBL_VESLE	BL_VESXA	S1_MYOSC	SMS_ALLMI	GTS_ASADI	NXSO_PSETE	PLAC_SHEEP	UC27_MAIZE	HBD_CLOPA	TL09_SPIOL	AKH_TABAT		RT34_BOVIN			HTF_HELZE	-	LM_TETTH
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P82690 periplaneta P04205 vespa manda				P82393 litoria ran P83187 basella alb	
PPK4 PERFU MAST VESMA	PH1 PRUSE GR78 HORSE	LEC3_AXIPO R13A_SPIOL	RKGG_CARCR	AU26_LITRA BRB BASAL	MMPX SOLTU PH2 PRUSE
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12	14 15	15	15	116	16
18.1	18.1	18.1	18.1	18.1	18.1
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3.34 5.05	36 37	8 6 6	40	4 4	4 4 4 7

ALIGNMENTS

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                                                              01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: On the 2D-gel the determined pl of this unknown protein is: 6, its Mw is: 15 kDa. SWISS-2DPAGE; P31929; HUMAN.
NON TER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
Pollen allergen Ory s 2-A (Fragment).
Oryza sativa (Rice).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                TISSUE-Liver;
MEDLINE=94147969; PubMed=8313870;
Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
"Human liver protein map: update 1993.";
Electrophoresis 14:1216-1222(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. Japonica; TISSUE=Pollen;
Kerim T., Imin N., Weinman J.J., Rolfe B.G.;
Submitted (SEP-2002) to Swiss-Prot.
-!- ALLERGEN: Causes an allergic reaction in human. Causes grass
pollen allergy. Bainds 1gE.
-!- SIMILARITY: Belongs to the expansin family.
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26.5%; Score 22; DB 1; Length 9;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 3; Conservative 3; Mismatches 3; Indels
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                                  9 AA.
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                                  PRT;
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                                  STANDARD;
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1 LVKKQTYHI 9
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                                  ULAD HUMAN
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RESULT 1
ULAD HUMAN
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MP2A_ORYSA
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Proc. Natl. Acad. Sci. U.S.A. 99:84-89(2002)
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Best Local Similarity
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9 VSYHVY 14
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OC Eukary
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MALT BACTO
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Purification of an acidic plastocyanin from Microcystis aeruginosa.",
Biochim. Biophys. Acta 973:111-117(1989)
-!-FUNCTION: Participates in electron transfer between P700 and the
cytochrome b6-f complex in photosystem I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21642653; PubMed=11756661; Eigenhear R.A., Nicolson S.W., Schegg K.M., Hull J.J., Schooley D.A.; Eigenhear R.A., Nicolson S.W., Schegg K.M., Hull J.J., Schooley D.A.; "Identification of a potent antidiuretic factor acting on beetle Malpighian tubules.";
                                                                                                                                                            Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Antidiuretic factor A (ADFa) (ADF) (Antidiuretic hormone A) (ADHA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.1%; Score 20; DB 1; Length 15; 50.0%; Pred. No. 2.1e+03; tive 1; Mismatches 3; Indels
                                                                                                                   Score 20; DB 1; Length 15;
Pred. No. 2.1e+03;
3; Mismatches 0; Indels
                                                                              2C65C9FBE3632A1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microcystis aeruginosa.
Bacteria; Cyanobacteria; Chroococcales; Microcystis.
NCBI_TaxID=1126;
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                                                                                                                                                                                                                                                                                                                                                                                 01-0701-1989 (Rel. 11, Created)
01-JUU-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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InterPro; IPR007112; Expan_endogl.
PROSITE; PS50842; EXPANSIN_EG45; FALSE_NEG
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InterPro; TPR000923; BlueCu 1.
PROSITE; PS00196; COPPER_BLÜE; PARTIAL.
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                                                                                                                 24.1%;
50.0%;
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1513 MW;
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                                                                                              Query Match
Query Match
Best Local Similarity 50.v.,
Best Local Similarity
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Best Local Similarity
                                                           15 AA;
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EVTFKV 7
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SEQUENCE
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SEQUENCE
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P82965;
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-i- FUNCTION: Strong inhibitor of fluid secretion by the Malpighian tubules. Uses CGMP as a second messenger and inhibits fluid production by decreasing cAMP concentration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001 (Rel: 40, Created)
Locr-2001 (Rel: 40, Last sequence update)
15-MAR-2004 (Rel: 43, Last amnotation update)
Phospholipase A2, basic 1 (EC 3.1.1.4) (PA2-1) (PLA2-1)
Phospholipase A2, basic 1 (EC 3.1.1.4) (PA2-1) (PLA2-1)
Chosphatidylcholine 2-acylhydrolase) (Fragment).
Trimeresurus stejnegeri (Chinese green tree viper).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eur. J. Biochem. 205:249-256(1992).
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
linked D-glucose residues with release of D-glucose.
-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
PIR; S21240; S21240.
Hydrolase; Glycosidase.
                                                                                                    -!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMEREX: MW=1541.58; METHOD=MALDI.
-!- SIMILARITY: STRONG, TO THE C-TERMINAL OF T.MOLITOR CUTICULAR
PROTEIN LPCP29.
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01-AUG-1992 (Rel. 23, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Maltase (S. 3.2.1.20) (Alpha-glucosidase I) (Fragment).
Bacillus thermoamyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                         GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005184; F:neuropeptide hormone activity; NAS.
GO; GO:0007218; P:neuropeptide signaling pathway; NAS.
                                                                                                                                                                                                                                                                                                                                             Neuropeptide, Hormone.
SEQUENCE 14 AA; 1543 MW; F49C91A3F16E43D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA; 1929 MW; 62B4CE501F2D3042 CRC64;
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33.3%; Pred. No. 3.2e+03;
tive 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              22.9%; Score 19; DB 1; 50.0%; Pred. No. 3e+03; tive 2; Mismatches
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Best Local Similarity 50.0
Matches 3; Conservative
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15 AA
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MEDLINE=98399821; PubMed=9729464;
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                                                                                                                   STANDARD;
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SYKPHIYG 12
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10-OCT-2003
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                                                                                                                                                                                                                                 (Fragment).
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                                                                                                       Li S. Y., Guo Z. -X., Yang Y. -Y., Wang W. -Y., Xiong Y. -L.;
"Isolation and sequencing of five variants of phospholipase A2
from women of snake Trimeresurus stejnegeri.";
J. Hubei Univ. 25:63-68(2003)
-!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
acyl groups in 3-sn-phosphoglycerides.
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
acylglycerophosphocholine + a fatty acid anion.
-!- COPACTOR: Binds I calcium ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eigenheer R.A., Wiehart U.M., Nicolson S.W., Schoofs L., Schegg K.M., Hull J.J., Schooley D.A.;
"Isolation, identification and localization of a second beetle antidiuretic peptide.";
Peptides 24:27-34 (2003).
-I- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses CAMP as second messenger. May function as an antidiuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two pairs of bilaterally symmetrical cells in the protocerebrum. MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI.
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                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
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 Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
40-OCT-2003 (Rel. 42, Last annotation update)
40.1 Autidiuretic factor B (ADP).
Tenebrio molitor (Yellow mealworm).
Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota, Tenebrionidae, Tenebrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.7%; Score 18; DB 1; Length 13; 37.5%; Pred. No. 4.2e+03; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.9%; Score 19; DB 1; Length 16; 66.7%; Pred. No. 3.4e+03; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                subfamily.
InterPro, IPR001211; PhospholipaseA2.
PROSITE; PS00119; PA2 ASP; PARTIAL.
PROSITE; PS00118; PA2—HIS; PARTIAL.
Hydrolase; Lipid degradation; Calcium; Multigene family.
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                   Viperidae; Crotalinae; Trimeresurus
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MEDLINE=22465067; PubMed=12576082;
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Lepidosauria; Squamata;
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Best Local Similarity
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                                   NCBI_TaxID=39682;
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                                                                                           TISSUE=Venom;
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P83109;
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                                                                        SEQUENCE
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RESULT 7

Matches

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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pyruvate dehydrogenase El component beta subunit, mitochondrial
(EC 1.2.4.1) (PDHEL-B) (Fragment).
Solanum tuberosum (Potato).
Enkaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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"Plant mitochondrial pyruvate dehydrogenase complex: purification and identification of catalytic components in potato.";
Biochem. J. 334:571-576 (1998).
-!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall conversion of pyruvate to acetyl-CoA and CO(2). It contains multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and lipoamide dehydrogenase (E3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                         Hoyt J.C., Johnson K.B., Reeves H.C.; "Purification and characterization of Acinetobacter calcoaceticus
                                                                                                                                                              Acinetobacter calcoaceticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter.
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-CCT-2003 (Rel. 42, Last amnotation update)
Isocitrate lyase (RC 4.1.3.1) (Isocitrase) (Isocitratase) (ICL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 173:6844-6848(1991).
-!- CATALYTIC ACTIVITY: Isocitrate = succinate + glyoxylate.
-!- PATHWAY: Glyoxylate bypass; first step.
-!- SUBJWIT: Homotetramer (By similarity).
-!- SUBJWIT: BOOCATION: Cytoplasmic.
-!- SUBILARITY: Belongs to the isocitrate lyase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 21.7%; Score 18; DB 1; Length 15; Local Similarity 75.0%; Pred. No. 4.8e+03; Pred. 3; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 AA; 1710 MW; 83AE726B1F2F96E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000918; Isocit lyase ph.
PROSITE; PS00161; ISOCITRATE LYASE; PARTIAL.
Glyoxylate bypass; Tricarboxylic acid cycle; Lyase.
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Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
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AC P13269,
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
Scombridae; Thunnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Wistar; TISSUE-Heart;
Li X.-P., Pleisener K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
Jungblut P.R.; Submitted (SEP-1998) to Swiss-Prot.
-!- SUBCELLUMAR LOCATION: Mitochondrial (Potential).
-!- MISCELLANGOUS: BY 2D-PAGE, the determined pI of this protein (spot
-!- P2) is: 8.9, its MW is: 25 kDa.
-!- SIMILARITY: BELONGS TO THE ESI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                         similarity)
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate; Nosphorylation; Mitochondrion.
NON TER
SEQÜENCE 16 AA; 1705 MW; FFGED80EC804F797 CRCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COXI THUOB STANDARD, PRT, 15 AA.
P80978;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Cytochrome c oxidase polypeptide VIC-2 (EC 1.9.3.1) (Fragments)
Thunnus obesus (Bigeye tuna).
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      -:- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-
acetylathydrolipoamide + CO(2).
-: COFACTOR: Thiamine pyrophosphate.
-:- CUPACTOR: Tretramer of two alpha and two beta subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.5%; Score 17; DB 1; Length 11; 75.0%; Pred. No. 5.40+03; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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11 AA; 1142 MW; D862272D32C72DC2 CRC64;
                                                                                                                                                                                                                                                                                                                                         21.7%; Score 18; DB 1; I
50.0%; Pred. No. 5.1e+03;
iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
115-MRA-2004 (Rel. 43, Last annotation update)
ES1 protein, mitochondrial (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AA
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MEDLINE=97454291; PubMed=9310366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                 Eur. J. Biochem. 248:99-103(1997).
-!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome coxidase, the terminal oxidase in mitochondrial electron transport.
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sex pheromone cPD1.

Enterococcus faecalis (Streptococcus faecalis).

Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

[1]
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Kadenbach B.; "The subunit structure of cytochrome-c oxidase from tuna heart
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                                                                                                                                                                                      c + 2 H(2)0.

-! SUBCELLULAR LOCATION: Mitochondrial inner membrane.

PIR; 877997; 877987.

Oxidoreductase; Inner membrane; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                            15 AA; 1696 MW; 4C4C966C73A40294 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Mollusca, Gastropoda, Pulmona
Sigmurethra, Achatinoidea, Achatinidae, Achatina.
NCBI_TaxID=6530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16; DB 1; I
Pred. No. 1.4e+05;
1; Mismatches 0
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01-07AN-1990 (Rel. 13, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Achatina fulica (Giant African snail).
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75.0%;
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Best Local Similarity 60.v.
". 3; Conservative
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Neuropeptide; Amidation.
MOD_RES 7 7
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TISSUE=Ganglion;
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2 KQMS 5
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SECUENCE

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Search completed: August 12, 2004, 07:04:05 Job time : 33 secs
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gong N.L., Armugam A., Jeyaseelan K.,

Gong N.L., Armugam A., Jeyaseelan K.,

"Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA
T. aloning, expression and protein characterization.";

Bur. J. Blochem. 265-982-989(1999)

-!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
acetylcholine receptors (nAchR).

-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- TASSUE SPECIFICITY: Expressed by the venom gland.
-!- MASS SPECIFICITY: Expressed by intravenous injection.
-!- MASS SPECIFICITY: Expressed by intravenous injection.
-!- SIMILARITY: Belongs to the snake toxin family.

RESITE, PSOUZZ; SNAKE TOXIN; PARTIAL.

RESITE, PSOUZZ; SNAKE TOXIN; PARTIAL.

TOXIN; Neurotoxin; Postsynaptic neurotoxin;
Acetylcholine receptor inhibitor; Multigene family.

UNSURE
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
             MEDLINE=85040388; PubMed=6436978;
Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
Craig R.A., Clewell D.B.;
"Isolation and structure of bacterial sex pheromone, cPDI.";
                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Short neurotoxin NI (Alpha neurotoxin) (Fragment).
Pseudonaja textilis (Eastern brown snake).
Braaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Acanthophiinae; Pseudonaja.
                                                                                                                                                                                                                .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                          Science 226.849-850(1984).
-!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF BACTERIOCIN PLASMID PPD1.
                                                                                                                                                                          19.3%; Score 16; DB 1; Length 8; 40.0%; Pred. No. 1.4e+05; Live 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.3%; Score 16; DB 1; Length 11; 75.0%; Pred. No. 8.1e+03; tive 0; Mismatches 1; Indels
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01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page (Spot 2D-000K2F) (Fragment).
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11 AA; 1319 MW; ODIEFOC81B58732B CRC64;
                                                                                                                                            8 AA; 913 MW; 8665B729C682C729 CRC64;
                                                                                                                                                                                                                                                                                                                                                            11 AA.
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MEDLINE=99449602; PubMed=10518793;
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                                                                                                                                                         Query Match
Best Local Similarity 40.07
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P59072;
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SEQUENCE
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NXSN PSETE
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Sanchez J.-C., Golaz O., Schaller D., Morch F., Frutiger S.,
Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;
Submitted (AUG-1995) to Swiss-Prot.
-!- MISCELLANEOUS: On the 2D-gel the determined pl of this unknown
protein is: 6.20, its MW is: 9.2 kDa.
SWISS-2DPAGE; P99013; YEAST.

NON_TER 11 11
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                     NCBI_TaxID=4932;
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Q9xlj8 grus leucog
Q9th03 grus paradi
Q8t6e9 drosophila
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Q35793 saccharomyc
Q95213 oryctolagus
Q91293 helicobacte
Q89129 borrelia bu
Q91575 synechocyst
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077900 oreochromis
077917 oreochromis
077912 oreochromis
077921 pseudotroph
077901 oreochromis
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                                                  August 12, 2004, 07:01:00 ; Search time 34 Seconds (without alignments) 157.759 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                         1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                    OM protein - protein search, using sw model
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Q9XL78
Q9XL78
Q9TG39
Q8ST15
Q35793
Q9S713
Q9R333
Q9R333
Q9R575
Q9R4G1
Q9R4G1
Q9R4G1
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Match Length DB
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ALIGNMENTS

STIVKOM 13

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RESULT 2

Q9XLJ8

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SEQUENCE FROM N.A.
Schaeffer S.W., Goetting-Minesky M.P., Kovacevic M., Peoples J.,
Schaeffer S.W., Goetting-Minesky M.P., Kovacevic M., Peoples J.,
Graybill J.L., Miller J.M., Kim K., Nelson J.G., Anderson W.W.;
"Evolutionary genomics of inversions in Drosophila pseudoobscura:
Modes of selection.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AA76817; AAL91815.1;
EMBL; AF476817; AAL91815.1;
NON TER
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                                                                                                                                                               Drosophila miranda (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.5%; Score 22; DB 5; Length 13; 36.4%; Pred. No. 5.4e+03; ive 4; Mismatches 3; Indels
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EMBL, AR476728; AAL91726.1; -.
EMBL, AR476730; AAL91727.1; -.
EMBL, AR476730; AAL91728.1; -.
EMBL, AR476731; AAL91729.1; -.
EMBL, AR476731; AAL91730.1; -.
EMBL, AR476733; AAL91730.1; -.
EMBL, AR476733; AAL91730.1; -.
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Q8STI5;
Q1-UTM-2002 (TrEMBLrel. 21, Created)
01-UTM-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Myocyte enhancing factor 2 (Fragment).
                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Mycoyte enhancing factor 2 (Fragment).
13 AA
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PRT;
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AAL91733.1;
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AAL91736.1;
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AAL91739.1;
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PRELIMINARY;
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AF476745; 1
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                         Q8T6E9
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Glenn T.C., Stephan W., Braun M.J.;
Glenn T.C., Stephan W., Braun M.J.;
Effects of a Population Bottleneck on Whooping Crane Mitochondrial
DNA Variation.";
Conserv. Biol. 0:0-01999).
EMBL; AR12371; AAD239921;
GO; GO:0005739; C:mitochondrion; IEA.
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Glenn T.C., Stephan W., Braun M.J.;
Glenn T.C., Stephan W., Braun M.J.;
"Effects of a Population Bottleneck on Whooping Crane Mitochondrial
DNA Variation.";
Conserv. Biol. 0.0-0(1999).
EMBL; AF112372; AAD23993.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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Wararyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Gruiformes; Gruidae; Grus.
NCBI_TaxID=40825;
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                    Archosauria, Aves, Neognathae, Gruiformes, Gruidae, Grus.
NCBI_TaxID=40819;
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Pred. No. 4.2e+03;
2; Mismatches 3; Indels
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Pred. No. 4.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion.

NON TER 15 15
SEQUENCE 15 AA; 1807 MW; A7FFB3A65E6A734F CRC64;
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SEQUENCE 15 AA; 1807 MW; A7FFB3A65E8A734F CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
NADH dehydrogenase subunit 6 (Fragment).
                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
NADH dehydrogenase subunit 6 (Fragment).
                                                                                 15 AA
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                                                                                                                                                                                                                                             ND6.
Grus leucogeranus (Siberian crane).
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27.7%;
Best Local Similarity 44.4%;
Matches 4; Conservative 2
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4; Conservative
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Grus paradisea (Blue crane)
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                                                                                 PRELIMINARY;
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1 MTYFMFFMG 9
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EMBL; AF476815; AAL91813.1; ---
EMBL; AF476816; AAL91814.1; ---
Flybase; FBGN0062298; Dpse\Mef2.
NON TER
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AAL91803.1; -.
AAL91804.1; -.
AAL91805.1; -.
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AAL91811.1; -.
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STRANN=F-1/rgm;
Mage R.G., Chen H.-T., Alexander C.B., Chen F.F.;
"Rabbit DGS2 and DH Gene Rearrangements in Early B-cell Development.";
Mol. Immunol. 0:0-0(1996).
EMBL; U62585; AAB18735.1; -.
NON_TER B 8
SEQÜENCE 8 AA; 845 MW; 5CA861B5AB58677B CRC64;
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Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=D273-10B;
MEDLINE=81069885; PubMed=6254986;
MEDLINE=81069885; PubMed=6254986;
Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
"Assembly of the mitochondrial membrane system: Structure and nucleotide sequence of the gene coding for subunit I of yeast cytochrome oxidase.";
                                                                                                                                                                                                                                                                                                                        Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                          Length 13;
                                       Score 22; DB 5; Length 13;
Pred. No. 5.4e+03;
4; Mismatches 3; Indels
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13 13
13 AA, 1749 MW, 114378726A89945B CRC64;
 13 AA; 1313 MW; 15BF380B6BE05050 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Inside intron 4 (Fragment).
Saccharomyces cerevisiae (Baker's yeast).
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Germline DH (DE) gene (Fragment).
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EMBL; V00694; CAA24065.1; -.
GG); GO:0005739; C:mitochondrion; IEA.
Mitochondrion.
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36.4%;
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                        Query Match
Best Local Similarity
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                                                                 Gaps
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
Urease large subunit (Fragment).
Helicobacter felis, and
Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NOBI_TaxID=214, 210;
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
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Turbett G.R., Hoj P.B., Horne R., Mee B.J.;
"Purification and characterization of the urase enzymes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21; DB 2; Length 12;
Pred. No. 7.5e+03;
4; Mismatches 2; Indels
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                      25.3%; Score 21; DB 7; Length 8; 50.0%; Pred. No. 1e+06;
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SEQUENCE 12 AA; 1500 MW; 93F05D2362132415 CRC64;
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13 AA; 1548 MW; 08E030E20078A32B CRC64;
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Last sequence update)
Last annotation update)
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Infect. Immun. 60:5259-5266(1992).
PIR; C49215; C49215.
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01-MAR.2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
Bdr protein (Fragment).
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Berger S., Ellersiek U., Kinzelt D., Steinmuller K.;

Berger S., Ellersiek U., Kinzelt D., Steinmuller K.;

"Immunopurification of a subcomplex of the NAD(P)H-plastoquinone-oxidoreductase from the cyanobacterium Synechocystis sp. PCG6803.";

PEBS Lett. 326:246-226(1993).

SEQUENCE 17 AA; 1890 MW; F776D9EFE2A58FF7 CRC64;
                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
NAD(P)H-plastoquinone-oxidoreductase 18 kDa polypeptide (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBL_TaxID=83334;
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BYR; G85802; G85802.
Hypothetical protein; Complete proteome.
SEQUENCE 9 AA. 1107 MW; 8F6CB72699D1BB41 CRC64;
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Last annotation update)
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  17 AA
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NCBL_TaxID=1142;
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STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
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PRT;
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                                                   01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2000 (TrEMBLrel. 14,
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Best Local Similarity 40.0
Best 4; Conservative
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PRELIMINARY;
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01-DEC-2001 (TEMBLIEL) 19, Last annotation update)
MHC class II B locus 14 (Fragment).
Creochromis niloticus (Nile tilapia) (Tilapia nilotica).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Cichidae; Oreochromis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98315113; PubMed=9649539; Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V., Figueroa F., Sultmann H., Klein J.; "Linkage relationships and haplotype polymorphism among cichlid mhc class II B loci."; Genetics 149:1527-1537(1998).

EMBL; AF050010; AAC41349.1; -.
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MEDLINE=98315113; PubMed=9649539;
Malaga=Trillo E., Zaleska-Rucczynska Z., McAndrew B., Vincek V.,
Melaga Trillo E., Sulmann H., Klein J.;
"Linkage relationships and haplotype polymorphism among cichlid mhc
class II B loci.";
Genetics 149:1527-1537(1998).
BMBL; AF050030; AAC41369.1; -.
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Pred. No. 1e+04;
2; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II B locus 14 (Fragment).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)
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01-NOV-1998 (TrEMBLrel. 08, Created)
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
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01-NOV-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II B locus 14 (Fragment).
Pseudotropheus sp. 'Pseudotropheus tropheops complex'.
Bukaryota, Metazoa, Chordara, Craniata, Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
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EMBL; AF050012; AAC41351.1; -.
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                              01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II B locus 14 (Fragment).

Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
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NCBI_TaxID=8128;
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3 MTYRL 7
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August 12, 2004, 07:04:56 ; Search time 41 Seconds (without alignments) 130.165 Million cell updates/sec
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508,
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-253-286-492

US-10-253-286-493

US-10-245-871-493

US-10-245-871-493

US-10-253-286-508

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US-10-253-286-501
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US-10-200-708-291
US-10-246-581-24
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                                                                                                                                                                                                                                               1292805 segs, 313927144 residues
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Maximum Match 100%
Listing first 45 summaries
                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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	Sequence 48, Appl Sequence 2292, Ap Sequence 34, Appl Sequence 11, Appl	38 21 13 27	28, 33, 60, e 32,	283,	444444
0 8 US-08-0 0 12 US-10 2 14 US-10 3 12 US-09	6 14 16 18 15 16 16 16 15 15 15 15 15 15 15 15 15 15 15 15 15	US-09-847-185- US-09-923-831- US-09-872-832- US-09-888-721-	9 US-09-888-721-2 9 US-09-766-889A- 9 US-09-909-460-6 10 US-09-898-860-		10-367-580 10-367-593 10-367-594 10-367-658 10-367-658
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ALIGNMENTS

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OTHER INFORMATION: sequence of interleukin-2 fragment (60-70) (T-cell growth factor)
RESULT 1

18-10-360

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 5; Conserv
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US-10-253-286-492
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LENGTH: 11
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NUMBER OF SEQ ID NOS: 905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Sequence 493, Application US/10253286 |
| Sequence 493, Application US/10253286 |
| Publication No. US20040058881A1 |
| GENERAL INFORMATION: HUMPHERS, ROBERT |
| APPLICANT: HUMPHERSY, ROBERT |
| APPLICANT: XU, MIXZHEN |
| TITLE OF INVENTION: I1-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES |
| FILE REFRENCE: REH-2015 |
| FURRENT APPLICATION NUMBER: US/10/253,286 |
| CURRENT FILING DATE: 2003-01-13 |
| PRIOR FILING DATE: 2002-07-17 |
| PRIOR FILING DATE: 1999-09-14 |
| PRIOR FILING DATE: 1999-09-14 |
| SEQ ID NOS: 905 |
| SOFTWARE: Patentin Ver. 2.1 |
| SEQ ID NO 493
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US-10-245-871-492

US-10-245-871-492

; Sequence 492, Application US/10245871
; Publication No. US20030235594a1
; GENERAL INFORMATION:
; APPLICANT: HUMPHERSY, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: I1-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: ERH-201;
; CURRENT FILING DATE: 2003-01-09
; PRIOR PILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR PILING DATE: 2002-07-17
; PRIOR PILING DATE: 1999-09-14
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APPLICANT: XU, MINZHEN
TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REPEREBNE: REH-2015
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 492
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Pred. No. 1.2e+06;
3; Mismatches 0; Indels
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Pred. No. 1.2e+06;
3; Mismatches 0;
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57.1%;
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CORGANISM: Homo sapiens
US-10-253-286-493
                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-253-286-492
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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1 IYMNGTM 7
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3 IYMNGTM 9
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Sequence 493, Application US/10245871

Publication No. US20030235594A1

SERBERAL INFORMATION:

APPLICANT: HUMPHERYS, ROBERT

APPLICANT: HUMPHERYS, ROBERT

TITLE OF INVENTION: II-KEX/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

FILE REFERENCE: RBH-2013

CURRENT APPLICATION NUMBER: US/10/245,871

CURRENT PILING DATE: 2003-01-09

PRIOR APPLICATION NUMBER: 09/197,000

PRIOR APPLICATION NUMBER: 09/296,813

PRIOR APPLICATION NUMBER: 09/296,813

PRIOR APPLICATION NUMBER: 09/296,813

PRIOR PRIOR OF SEQ ID NOS: 905

SEQ ID NO 493

SEQ ID NO 493
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                                                                                                              Length 9;
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Pred. No. 1.2e+06;
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57.1%;
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 492
LENGTH: 9
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Best Local Similarity 57.1
Matches 4; Conservative
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US-10-245-871-493
                                                                , ORGANISM: Homo sapiens
US-10-245-871-492
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Best Local Similarity
Matches 4; Conserv
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1 IYMNGTM 7
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NAME/KEY: MOD_RES
LOCATION: (5)
OTHER INFORMATION: a-aminovaleric acid
                                                                                                                                                                                                                                       OTHER INFORMATION: a-aminovaleric acid
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Publication No. US20030235594A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: C-term amidated US-10-245-871-508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: C-term amidated US-10-245-871-509
                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 57.11
Best Local 4; Conservative
        NUMBER OF SEQ ID NOS: 905
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
Matches 4; Conserv
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LOCATION: (5)
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US-10-253-286-501
                                                SEQ ID NO 508
                                                                    LENGTH: 14
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APPLICANT: TO MINZHEN
TITLE OF INVENTION: 1.1-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2015
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT FILING DATE: 2003-01-13
FRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOSTWARE: PACENTIN VEY: 2.1
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Publication No. US200302355941

GENERAL INPORMATION:

APPLICANT: HUMPHREYS, ROBERT

APPLICANT: HUMPHREYS, ROBERT

TITLE OF INNVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

FILE REFERENCE: REH-2013

CURRENT APPLICATION NUMBER: US/10/245,871

CURRENT APPLICATION NUMBER: 10/197,000

PRIOR APPLICATION NUMBER: 09/396,813

PRIOR FILING DATE: 2002-01-77

PRIOR FILING DATE: 1999-09-14
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Ii-Key/tyrosinase overlapping hybrid peptide
FEATURE:
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                                                                                                                                                       33.7%; Score 28; DB 12; Length 14; 57.1%; Pred. No. 2.7e+02; tive 3; Mismatches 0; Indels
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FEATURE:
NAME/KEX: MOD_RES
LOCATION: (5)
OTHER INFORMATION: a-aminovaleric acid
FEATURE:
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LOCATION: (5)
OTHER INFORMATION: a-aminovaleric acid
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                                                                                            ) OTHER INFORMATION: C-term amidated US-10-253-286-508
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Best Local Similarity 57.15
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8 IYMNGTM 14
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APPLICANT: WINZHEN
TITLE OF INVENTION: I1-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2013
CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT FILING DATE: 2003-01-09
PRIOR PILING DATE: 2002-01-09
PRIOR PILING DATE: 1999-09-14
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 965
SOFTWARE: PALENTIN VER. 2.1
SEQ ID NO 509
LENGTH: 14
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: 11-Key/tyrosinase overlapping hybrid peptide
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Gaps

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Sequence 510, Application US/10245871

Publication No. US20030235594A1

GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REPRENCE: REH-2013
CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT APPLICATION NUMBER: 10/197,000
PRIOR PILING DATE: 2002-01-09
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PATENTIN VENER: 09/396,813
FRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SEQ ID NO 510
MANDET NO 510
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      TITLE OF INVENTION:

TITLE OF INVENTION:

FILL REPERENCE: REH-2013

CURRENT APPLICATION NUMBER: US/10/245,871

CURRENT PILING DATE: 2003-01-09

PRIOR APPLICATION NUMBER: 09/396,813

PRIOR APPLICATION NUMBER: 09/396,813

PRIOR APPLICATION NUMBER: 09/396,813

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 905

SOFTWARE: PARENTIN Ver. 2.1

SEQ ID NO 501
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Pred. No. 3.4e+02;
3; Mismatches 0; Indels
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57.1%;
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US-10-245-871-501
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4 IYMNGTM 10
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Best Local Similarity
Matches 4; Conserv
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NAME/KEY: MOD_RES
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APPLICANT: HUMPHRES, ROBERT
APPLICANT: HUMPHRES, ROBERT
TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: EBH-2018
CURRENT APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2003-01-13
PRIOR PILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 510
LINGS APPLICATION OF 2.1
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APPLICANT: XU, MINZHEN
TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REPERENCE: REH-2015
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT PILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PALCHIN VET. 2.1
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Pred. No. 3.4e+02;
3; Mismatches 0;
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; Sequence 501, Application US/10245871
; Publication No. US20030235594A1
; SRNERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 510, Application US/10253286; Publication No. US20040058881A1; GENERAL INFORMATION:
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57.1%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 57.1.
Thes 4; Conservative
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ORGANISM: Homo sapiens
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9 IYMNGTM 15
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                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 501
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 17
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OTHER INFORMATION: protein sequence for GFPm to ZmRAD51B fusion,

OTHER INFORMATION: inlcuding isoleucine and histidine linker
US-10-246-581-24
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TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WS-10-146-581-24
Sequence 24, Application US/10246581
Sequence 24, Application US/10246581
Sequence 24, Application US/10246581
GENERAL INFORMATION:
APPLICANT: Bowen, Benjamin A.
APPLICANT: Drummond, Bruce J.
APPLICANT: Drummond, Bruce J.
APPLICANT: McElver, John A.
APPLICANT: Rothstein, Rodney J.
TITLE OF INVENTION: RAD51 Polypeptides
FILE REFERENCE: 0556D
CURRENT APPLICATION NUMBER: US/10/246,581
CURRENT APPLICATION NUMBER: US 09/246,963
PRIOR APPLICATION NUMBER: US 09/246,963
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24
               FILE REFERENCE: 17999-001

CURRENT APPLICATION NUMBER: US/10/200,708

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: US/09/351,036

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-10

PRIOR APPLICATION NUMBER: 60/115,145

PRIOR APPLICATION NUMBER: 60/115,145

PRIOR APPLICATION NUMBER: 60/115,145

PRIOR APPLICATION NUMBER: 60/130,677

PRIOR PILING DATE: 1999-04-23

NUMBER OF SEQ ID NOS: 672

SOFTWARE: PACENTIN VET: 2.1

SEQ ID NO 291
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                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Human immunodeficiency virus US-10-200-708-291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 57.1
Matches 4; Conservative
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Sequence 192
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-207-444-3

PCT-USS-0-5534-2

US-09-528-200-40

US-09-528-200-33

US-09-528-200-35

US-09-528-200-19

US-09-528-200-19

US-09-528-200-19

US-09-528-200-12

US-09-528-200-11

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Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 17
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Match
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Result No.

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288, 484, 1191, 122, 123, 13, 13, 13, 13,		, ca,	
Sequence Sequence		INCREASED 5691162th America,	Length 14;
		US/08443104 Useffrey R. Anna L. Claus Sven NOVEL METALLOPROTEASE HAVING ACTIVITY 10 Ss: 11620 No. 5691162disk of No. Iton Avenue, 64th Floor Icompatible PC-DoS/MS-DOS IRElease #1.0, Version #1.25 US/08/443,104 IS-1995 ATA: US 08/396,489 RTION: Heryl H. Is 34,086 MBER: 4180.010-US ORMATION: Heryl H. Is 34,086 MBER: 4180.010-US ORMATION: G55 NO: 2: Cids ICC:	Len
US-09-528-200-28 US-09-528-200-34 US-09-528-200-46 US-09-528-200-46 US-09-528-200-191 US-09-528-200-21 US-09-528-200-27 US-09-528-200-27 US-09-528-200-27 US-09-528-200-14 US-09-528-200-14 US-09-528-200-14 US-09-528-200-14 US-09-528-200-14 US-09-528-200-14 US-09-528-200-14 US-09-528-200-13 US-09-528-200-13 US-09-528-200-13 US-09-528-200-13 US-09-528-200-13 US-09-528-200-13 US-09-528-200-13 US-09-528-200-13 US-09-528-200-13 US-09-528-200-13		HAV	1;
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		-2 Applicable Applicab	ı Similarity
		Squence 2, Application 1 squence 2, Application 1 squence 2, Application 1 APPLICANT: Shuster, APPLICANT: Madden, M APPLICANT: Madden, M APPLICANT: Moyer, Don APPLICANT: Moyer, Don APPLICANT: Moyer, Don APPLICANT: Moyer, Don APPLICANT: Branner, TITLE OF INVENTION: N TITLE OF INVENTION: N TITLE OF INVENTION: N TITLE OF INVENTION: N TITLE OF INVENTION: N TITLE OF INVENTION: N STREET: New York COUNTRY: USA ZIP: 10174-6401 COMPUTER: READABLE FORM MEDIUM TYPE: TAMPEC COMPUTER: IBM PC COMPUTER: BEADABLE FORM MEDIUM TYPE: TAMPEC COMPUTER: BEADABLE FORM MEDIUM TYPE: TAMPEC COMPUTER: BEADABLE FORM MEDIUM TYPE: TAMPER: PLILING DATE FILING DATE: 17-MAX CLIASSIFICATION DATE APPLICATION NUMBER: FILING DATE: 33-MAX ATTORNEY/AGENT INFORM NAME: Agris DT. C REGISTRATION FOR SEQ ID N SECONMUNICATION INPET TELEPHONE: 212-867- LENGTH: 14 amino acid STRANDENBESS: Singl TOPOLOGY: linear MOJECULE TYPE: PEPLIGA	th Sin
		J.T. 1 J. 443-104 Jubence 2, ent in Applican APPLICAN APPLICAN APPLICAN APPLICAN TITLE OF TIT	/ Match Local S
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1 US-08-443-104-2 Sequence 2, Applicati Sequence 2, Applicati Sequence 2, Applicati Sequence 2, Applicati Sequence 2, Applicati APPLICANT: Shuste APPLICANT: Madden APPLICANT: Madden APPLICANT: Branne TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TOWNOTE : 405 Lex COUNTRY: USA ZIP: 10174-6401 COMPUTER: New YORK COUNTRY: USA ZIP: 10174-6401 COMPUTER: READABLE MEDIUM TYPE: TA COMPUTER: BM P SOFTWARE: PAECO CURRENT APPLICATION APPLICATION NUMB FILING DATE: 17 CLASSIFICATION APPLICATION NUMB FILING DATE: 03 ATTORNEY/AGENT INF NAME: APPLICATION NUMB FILING DATE: 03 ATTORNEY/AGENT INF REFERENCE/DOCKET TELEPHONE: 212-87 INFORMATION FOR SEQ SEQUENCE CHARACTER: LENGTH: 14 amind TELEPHONE: 212-87 INFORMATION FOR SEQ SEQUENCE CHARACTER: LENGTH: 14 amind TELEPHONE: 212-87 INFORMATION FOR SEQ SEQUENCE CHARACTER: LENGTH: 14 amind TELEPHONE: 212-87 INFORMATION FOR SEQ SEQUENCE CHARACTER: LENGTH: 14 amind TELEPHONE: 212-87 INFORMATION FOR SEQ SEQUENCE CHARACTER: LENGTH: 14 amind TELEPHONE: 212-87 INFORMATION FOR SEQ SEQUENCE CHARACTER: LENGTH: 14 amind TELEPHONE: 212-87 INFORMATION FOR SEQ SEQUENCE CHARACTER: LENGTH: 14 amind TELEPHONE: 212-87 INFORMATION FOR SEQ SEQUENCE CHARACTER: LENGTH: 14 amind TELEPHONE: 212-87 INFORMATION FOR SEQ SEQUENCE CHARACTER: LENGTH: 14 amind TELEPHONE: 212-87 INFORMATION FOR SEQ SEQUENCE CHARACTER: LENGTH: 14 amind TELEPHONE: 212-87 INFORMATION FOR SEQ	Query Best L
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E: No. 58437530 No. 5843753disk of No. 5843753th America, Inc.
405 Lexington Avenue, 64th Floor
                                                                                                                                       ADDRESSEE: No. 58077290 No. 5807729disk of No. 5807729th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CIIY: New York
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US-08-399-489-2
Sequence 2, Application US/08398489
Sequence 2, Application US/08398489
Fatent No. 5843753
GENERAL INFORMATION:
APPLICANT: Shuster, Jeffrey R.
APPLICANT: Moden, Mark
APPLICANT: Moyer, Donna L.
APPLICANT: Healsang, Claus
APPLICANT: Branner, Sven
TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING INCREASED
TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58437530 No. 5843753disk of No. 5843753th Ame
                                      Fuglsang, Claus
Branner, Sven
VERNION: NOVEL METALLOPROTEASE HAVING INCREASED
VENTION: ACTIVITY
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Pred. No. 42;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                        OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,859
FILING DATE: 17-MAY-1995
CLASSIFICATION: 25.2
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/398,489
FILING DATE: 03=MAR-1995
ATTOMNEY/AGENT INPORMATION:
NAME: AGTIS DY., Cheryl H.
REGISTRATION NUMBER: 34,086
                                                                                                                                                                                                                                                                                                       3: Tape
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 411
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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                Moyer, Donna L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 14 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                   APPLICANT: Moyer, Donna APPLICANT: Puglsarg, Clt APPLICANT: Branner, Sver TITLE OF INVENTION: NOVE TITLE OF INVENTION: ACT NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
Madden, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
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MEDIUM TYPE: Tape
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STATE: New York
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10174-6401
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  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: No. 57029340 No. 5702934disk of No. 5702934th America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York STATE: New York
  Gaps
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34.9%; Score 29; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 2; Indels
    2; Indels
                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PUGISSES FOR PRODUCING AN ENZYME NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: ADDRESSES: NO. 670^^^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENTING SISIEM: TO-LOCAL MARCHING SISIEM: CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,130
FILING DATE: 04-MAY-1994
CLASSIFICATION TAX-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: DK 522/93
FILING DATE: 05-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Agris Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
APPLICATION NUMBER: 34,086
APPLICATION NUMBER: 34,086
APPLICATION NUMBER: 34,086
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3965.200-US
                                                                                                                                                                                                                                                                     Branner, Sven
Jozgensen, Birthe R.
Christensen, Tove
Jorgensen, Birgitte B.
Shuster, Jeffrey R.
Madden, Mark
Moyer, Donna L.
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                                                                                                                                                                                        Sequence 3, Application US/08238130 Patent No. 5702934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 396:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Tage
COMPUTER: IBM PC compatible
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        6; Conservative
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                                                8 TYKVYMSG 15
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                                                                                    TYKVYPWG 9
                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-238-130-3
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                                                                                                                                                  RESULT 2
US-08-238-130-3
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        Matches
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Gaps

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Host Cell Expressing Reduced Levels
Of A Metalloprotease And Methods Using The Host Cell In Proteir
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
Production
NUMBER OF SEQUENCES:
10
CORRESPONDENCE ADDRESS:
ADDRESSEE:
ADDRESSEE:
NO. 59687740 No. 5968774disk of No. 5968774th America,
STREET:
New York
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                                                                                                                                    Score 29; DB 2; Length 14; Pred. No. 42; 2; Indels 0; Mismatches 2; Indels
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Pred. No. 42;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/207,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,772
FILING DATE: 27-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, valeta A.
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 4300.204-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: U.S.A.
ZIP: 10.14-640.1
COMPUTER READABLE PORM:
MEDIUM TYPE: FLORPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                           US-09-207-844-3
Sequence 3, Application US/09207844
Patent No. 596874
GENERAL INFORMATION:
                                                                                                                                    34.9%;
ilarity 75.0%;
Conservative C
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INFORMATION FOR SEQ ID NO: 3:
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Similarity 75.0%;
6; Conservative
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LENGTH: 14 amino acids
                                                                  ; MOLECULE TYPE: peptide US-08-894-772-3
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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                                                 TOPOLOGY:
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PCT-US95-05534-2
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APPLICANT:
APPLICANT:
TITLE OF INVENTION: Host Cell Expressing Reduced Levels
TITLE OF INVENTION: Production
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58612800 No. 5861280disk of No. 5861280th America, Inc.
STREET: AGS Lexington Avenue, Suite 6400
CITY: New York
STREET: New York
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COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/894,772
FILING DATE: 27-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION TABE:
FILING DATE: APPLICATION DATA:
APPLICATION PATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 2; Length 14; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
CURRENT APPLICATION DATA:
PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
PTILING DATE: 03-MAR-1995
CLASSIFICATION: 43*
PTONNEY/AGFWT
CLASSIFICATION: 43*
                                                                                                                                                                                   ATTORNEY/AGENT INPORMATION:

NAME: AGIIS Dr., Cheryl H.

REGISTRATION NUMBER: 34,086

REFERENCE/DOCKET NUMBER: 4180.010-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEPA. 212-879-9655

INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 4300.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-08-894-772-3
Sequence 3, Application US/08894772;
Patent No. 5861280
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Best Local Similarity 75.0%;
Matches 6; Conservative
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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US-08-398-489-2
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STRANDEDNESS: siz
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US-08-413-708B-6
Sequence 6, Application US/08413708B
Sequence 6, Application US/08413708B
Sequence 6, Application US/08413708B
Sequence 6, Application US/08413708B
Sequence 6, Application US/08413708B
Septicant: GOZES, Illana
APPLICANT: GOZES, Illana
APPLICANT: FRIDATION: PHARMACHITCAL COMPOSITIONS COMPRISING
TITLE OF INVENTION: PHARMACHITCAL COMPOSITIONS COMPRISING
TITLE OF INVENTION: VIP, OR ANALOGUES DERIVATIVES AND FRAGMENTS THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESS
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Pred. No. 59;
                                                                                                                                                                                                                                                                             33.7%; Score 28; DB 4; Length 12; illarity 41.7%; Pred. No. 54; Conservative 3; Mismatches 4; Indels
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CUNDARY: USA
ZIP: 2004
ZIP: 2004
COMPUTER READBLE FORM:
MEDIUM TYPE: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,708B
FILING APPLICATION: 424
PRIOR APPLICATION TARE:
PRIOR APPLICATION UNBER: US/08/207,671
FILING DATE: 09-MAR-1994
PRIOR APPLICATION NUMBER: 11.105061
FILING DATE: 09-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
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TELEPHONE: 202-628-5197
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Best Local Similarity 38.5%;
Matches 5; Conservative
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    SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 IAKOMTYKVYMS 14
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                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washing
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                             US-09-528-200-40
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                                                   SEQ ID NO 40
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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NOVEL METALLOPROTEASE HAVING INCREASED ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.9%; Score 29; DB 5; Length 14; 75.0%; Pred. No. 42; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPANIES THAN TO COMPANIES OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05534
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238/108
FILING DATE: 04-MAY-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/398,489
FILING DATE: 03-MARCH-1995
CLASSIFICATION:
ATTCRNEY/AGENT INFORMATION:
NAME: AGIST CATION:
NAME: AGIST CATION:
NAME: AGIST CATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 4180.204-WO
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION                                                                                                                                                                         E: Novo Nordisk of North America, Inc. 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: SCH-1731
CURRENT APPLICATION NUMBER: US/09/528,200
CURRENT FILING DATE: 2000-03-17
PRICR APPLICATION NUMBER: DE 199 17 713.9
PRIOR FILING DATE: 1999-09-04
NUMBER OF SEQ ID NOS: 196
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Patent No. 6630570
GENERAL INFORMATION:
APPLICANT: LICHA, KAI
APPLICANT: BECKER, ANDREAS
APPLICANT: BECKER, WOLFHARD
APPLICANT: WEIDENMANN, BERTRAM
APPLICANT: WEIDENMANN, BERTRAM
APPLICANT: SCHNEIDER-ENGERT, RUDOLF
APPLICANT: SCHNEIDER-MERGENER, JENS
APPLICANT: BHARGRYA, STRAH
APPLICANT: BHARGRYA, STRAH
APPLICANT: BHARGRYA, STRAH
                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 amino acids
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Matches 6; Conservative
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        TITLE OF INVENTION: NOVE
TITLE OF INVENTION: ACTI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVO NOIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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STRANDEDNESS: siz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYKVYPWG 9
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                                                                                                                                                                                                                                                                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-09-528-200-40
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APPLICANT: BECKER, ANNREAS
APPLICANT: SEMMLER, WOLFHARD
APPLICANT: SEMMLER, WOLFHARD
APPLICANT: WEIDENMANN, BERTRAM
APPLICANT: HESSNIUS, CARTEEN
APPLICANT: SCHNIUDER-MERGENER, JENS
APPLICANT: SCHNIUDER-MERGENER, JENS
APPLICANT: SCHNIUDER-MERGENER, JENS
APPLICANT: SCHNIUDER-MERGENER, JENS
APPLICANT: SCHNIUDER-MERGENER, JENS
APPLICANT: SCHNIUDER-MERGENER, JENS
APPLICANT: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS
TITLE REFERENCE: SCH-1731
CURRENT APPLICATION NUMBER: US/09/528,200
CURRENT APPLICATION NUMBER: US/09/528,200
CURRENT APPLICATION NUMBER: DE 199 17 713.9
PRIOR FILING DATE: 1999-09-04
NUMBER OF SEQ ID NOS: 196
SOFTMARE: PATENTI VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HESSNIUS, CARTERN
APPLICANT: VOLKMER-ENGERT, RUDOLF
APPLICANT: SCHHEADER-ENGERER, JENS
APPLICANT: SCHHEADER-ENGERER, JENS
APPLICANT: HERGENER, JENS
TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: peptide US-09-528-200-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.7%; Score 28; DB 4; Length 14;
41.7%; Pred. No. 65;
ative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28; DB 4; Length 14;
Pred. No. 65;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: SCH-1731
CURRENT APPLICATION NUMBER: US/09/528,200
CURRENT FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: DE 199 17 713.9 STRIOR FILTING DATE: 1999-09-04 NUMBER OF SEQ ID NOS: 196 SOFTWARE: PATENTIN VEY. 2.1
                                                                                         Sequence 26, Application US/09528200 Patent No. 6630570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-528-200-32
; Sequence 32, Application US/09528200
; Patent No. 6630570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LICHA, KAI
APPLICANT: BECKER, ANDREAS
APPLICANT: SEMMLER, WOLDERARD
APPLICANT: WEIDENMANN, BERTRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 33.7%;
Best Local Similarity 41.7%;
Matches 5; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LRKOMAVKKYLN 12
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Best Local Similarity
'Lnc 5; Conserve
                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LICHA, KAI
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                                                                  US-09-528-200-26
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LENGTH: 14
TYPE: PRT
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BECKER, ANDREAS

..erlicant: BECKER, ANDREAS

APPLICANT: SEMELER, WOLFHARD

APPLICANT: WEIDENMANN, BERTRAM

APPLICANT: WEIDENMANN, BERTRAM

APPLICANT: WOLKWER-ENGERT, RUDOLF

APPLICANT: SCHNEIDER-MERGENER, JENS

APPLICANT: SCHNEIDER-MERGENER, JENS

APPLICANT: SCHNEIDER-MERGENER, JENS

APPLICANT: SCHNEIDER-MERGENER, JENS

APPLICANT: SCHNEIDER-MERGENER, JENS

TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA

TITLE OF INVENTION: POR OPTICAL DIAGNOSIS

TITLE OF INVENTION NUMBER: US/09/528,200

CURRENT FILING DATE: 1999-09-04

NUMBER OF SEQ ID NOS: 196

SOFTWARE: PATENTIN VET. 2.1

LENGTH: 13

LENGTH: 13

TYPE: re-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HESSNIUS, CARTSEN

ALPLICANT: HESSNIUS, CARTSEN

APPLICANT: OLIKHER-ENGERT, RUDOLF

APPLICANT: SCHNEIDER-MERGENER, JENS

APPLICANT: SCHNEIDER-MERGENER, JENS

TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS

FILE REFERENCE: SCH-1731

CURRENT APPLICATION NUMBER: US/09/528,200

CURRENT APPLICATION NUMBER: DE 199 17 713.9

PRIOR FILING DATE: 1999-09-04

SOFTWARE: PATENTIN OF: 2.1

SEQ ID NO 39

LENGTH: 13

TYPE: nr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
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Pred. No. 5
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41.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 41.7
Matches 5; Conservative
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1 LRKQMAVKKYLN 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
// ORGANISM: Homo sapiens
US-09-528-200-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-09-528-200-39
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Best Local Similarity
Matches 5; Conserv
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US-09-528-200-39
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Gaps

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Gaps

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PUBLICATION INFORMATION: AUTHORS:
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JOURNAL:
US-08-486-721A-16
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                                                                                    RESULT 14
US-08-486-721A-16
is Sequence 16, Application US/08486721A
is Patent No. 5739025
is Patent No. 5739025
is TUTLE OF INVENTION:
is TITLE OF INVENTION: Method of Producing
is TITLE OF INVENTION: Asparaginyl Endoprotease
is CORRESPONDENCE ADDRESS:
is ADDRESSEE: Frishauf, Holtz, Goodman, Langer & Chick
street: 767 Third Avenue
                                                                                                                                                                                                                                                                                                             STREET: 767 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
COMPUTE: NOAT -2023
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3+ inch, 1.4 mb
COMPUTER: EN FORTE: Diskette, 3+ inch, 1.4 mb
COMPUTER: SYSTEM: MS DOS
SOFTWARE: ASCIE:
APPLICATION DATA:
APPLICATION NUMBER: US/08/486,721A
FILING DATE: 7-JUNE-1995
FILING DATE: 7-JUNE-1995
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 08/091,991
FILING DATE: 12-JULY-1993
ATTORNEY/AGENT INFORMATION:
NAME: BARCH ACCHET UNBER: 28,180
REFERENCE/POCKET UNBER: 29,180
REFERENCE/POCKET UNBER: 29,180
TELLECOMMUNICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
TELLESTAX: (212) 319-4900
TELLESTX: 233268
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE: CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
                            : | | | | | ::
LRKOMAVKKYLN 13
  IAKOMTYKVYMS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNITS:
                                       dd
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GENERAL INFORMATION:
APPLICANT: LICHA, KAI
APPLICANT: LICHA, KAI
APPLICANT: BECKER, WOLFHARD
APPLICANT: BERMIER, WOLFHARD
APPLICANT: WEIDENWANN, BERTRAM
APPLICANT: WEIDENWANN, BERTRAM
APPLICANT: WEIDENWANN, BERTRAM
APPLICANT: WEIDENWANN, BERTRAM
APPLICANT: WINDER-ENGERT, RUDOLF
APPLICANT: SCHNEIDER-MERGENER, JENS
APPLICANT: BHARGAVE, SARAH
TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS
TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS
TITLE OF INVENTION WUMBER: US/09/528,200
CURRENT APPLICATION NUMBER: US/09/528,200
CURRENT APPLICATION NUMBER: DE 199 17 713.9
PRIOR FILING DATE: 1999-09-04
NUMBER OF SEQ ID NOS: 196
SEQ ID NO 19
LENGTH: 15
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Score 28; DB 1; Length 15;
Pred. No. 70;
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108-09-528-200-19
'Sequence 19, Application US/09528200
'Patent No. 6630570
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  33.7%;
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Best Local Similarity 41.7
Matches 5; Conservative
Query Match
Best Local Similarity 41.7
Matches 5; Conservative
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